

Result No.	Score	Query Match	Length	DB	ID	Description
1	432	100.0	432	2	QV785690	Sequence
2	432	100.0	432	4	AY692896	Saccharom
3	432	100.0	718	4	SA5268	TTR-thioltr
4	432	100.0	932	2	AX536532	Sequence
5	432	100.0	72119	4	SCD9717	Saccharomy
6	151.6	35.1	110000	4	CR3809957_05	Continuation (6 of)
7	147.4	34.1	833	2	AX536464	Sequence
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9	147	34.0	994	7	CNS060347	AL401117 T7 and of
10	143.4	31.2	333	2	QV785688	Sequence
11	137.6	31.9	110000	4	CR382123_00	Cluyverom
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13	89	20.6	360	2	AX489480	Sequence
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15	83.8	19.4	110000	4	CR382129_06	Continuation (7 of)
16	80.2	18.6	110000	4	AEQ16819_17	Continuation (18 of)
17	75.2	17.4	183	2	AR548880	Sequence
18	69.8	16.2	582	2	AR548881	Sequence

by

51 GCCACAAGAAATTATTCCTAAAGATTTTATCTACTCCAAAATGGTATCCCAGGAACA 1

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ORIGIN

Query Match 100.0%; Score 432; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 5e-123;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGACCAATTTTCTCGACTCGAATTTAATTTGTTATTTATCATTCACGTTGTTT 60
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DB 168 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 227

QY 121 GTTGCTCAGTAAGGATCTGATGGCCAAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
DB 228 GTTGCTCAGTAAGGATCTGATGGCCAAAAGAAAGTGTGTTGTCAGCAAGACATAC 287

QY 181 TGCCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 240
DB 288 TGCCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 347

QY 241 AAGGCCCTTGTGTTGGAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
DB 348 AAGGCCCTTGTGTTGGAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 407

QY 301 GAAGAAATCTCGGCCCAAAAACTGTACCTAACTATACATCAATGCGCAAGACATTTGGT 360
DB 408 GAAGAAATCTCGGCCCAAAAACTGTACCTAACTATACATCAATGCGCAAGACATTTGGT 467

QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
DB 468 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 527

QY 421 GTATTTCATATAG 432
DB 528 GTATTTCATATAG 539

RESULT 4
AX536532
LOCUS AX536532
DEFINITION Sequence 133 from Patent WO02064766.
ACCESSION AX536532
VERSION AX536532.1
KEYWORDS GI:25262936
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE 1
Contreras, R.H., Eberhardt, I., Luyten, W.H. and Reekmans, R.J.
TITLE Bax-responsive genes for drug target identification in yeast and fungi
JOURNAL Patent: WO 02064766-A 133 22-AUG-2002;
JANSEN PHARMACEUTICA N.V. (BE)
FEATURES
Location/Qualifiers
source 1..932

/organism="Saccharomyces cerevisiae"
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ORIGIN

Query Match 100.0%; Score 432; DB 2; Length 932;
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Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 120
DB 561 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAACA 620

QY 121 GTTGCTCAGTAAGGATCTGATGGCCAAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
DB 621 GTTGCTCAGTAAGGATCTGATGGCCAAAAGAAAGTGTGTTGTCAGCAAGACATAC 680

QY 181 TGCCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 240
DB 681 TGCCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAAGATTTGAACGTTCCCAATCC 740

QY 241 AAGGCCCTTGTGTTGGAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
DB 741 AAGGCCCTTGTGTTGGAATTTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 800

QY 301 GAAGAAATCTCGGCCCAAAAACTGTACCTAACTATACATCAATGCGCAAGACATTTGGT 360
DB 801 GAAGAAATCTCGGCCCAAAAACTGTACCTAACTATACATCAATGCGCAAGACATTTGGT 860

QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
DB 861 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 920

QY 421 GTATTTCATATAG 432
DB 921 GTATTTCATATAG 932

RESULT 5
SCD9717
LOCUS SCD9717
DEFINITION 72119 bp DNA linear
Saccharomyces cerevisiae chromosome IV cosmids 8166, 9787, 9717,
and lambda 3073.
ACCESSION U33057
VERSION U33057.1
KEYWORDS GI:927764
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE 1
Dietrich, F.S., Mulligan, J., Allen, E., Araujo, R., Aviles, E.,
Berno, A., Carpenter, J., Chen, E., Cherry, J.M., Chung, E., Duncan, M.,
Hunnicke-Smith, S., Hyman, R., Komp, C., Lashkari, D., Lew, H., Lin, D.,
Mosedale, D., Nakahara, K., Namath, A., Oefner, P., Oh, C., Petel, F.X.,
Roberts, D., Schramm, S., Schroeder, M., Shogren, T., Shroff, N.,
Winant, A., Yelton, M., Botstein, D. and Davis, R.W.
TITLE The sequence of Saccharomyces cerevisiae chromosome IV right
JOURNAL Unpublished (1995)
REFERENCE 2
Dietrich, F.S.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1995) Department of Genetics, Stanford
University, Stanford, CA 94305-5120, USA
REFERENCE 3
Jia, X. and Cherry, J.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1997) Department of Genetics, Stanford
University, Saccharomyces Genome Database, Stanford, CA 94305-5120,

COMMENT	USA	Sequenced by: Stanford DNA Sequence & Technology Center 855 California Avenue Palo Alto, CA 94304, USA
Curated by: Saccharomyces Genome Database		URL: http://genome-www.stanford.edu/yeast e-mail: yeast-curator@genome.stanford.edu
Neighboring Sequence:		The 5' end of this sequence contains a 550 bp overlap with GenBank Accession Number J3050. The 3' end is estimated to be 8 kb from the first of at least three subtelomeric Y' elements on the right telomere of chromosome IV.
FEATURES	Location/Qualifiers	
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source	1..41836 /organism="Saccharomyces cerevisiae" /mol_type="genomic DNA" /db_xref="taxon:4932" /clone="cosmid 9787"	
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CDS	complement(387..3422) /gene="VPS3" /note="YDR495C" /codon_start=1 /product="Vps3p: Vacuolar sorting protein" /protein_id="AAB64937.1" /db_xref="GI:927765"	
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gene complement(12470..13125)
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Query Match	100.0%;	Score 432;	DB 4;	Length 72119;
Best Local Similarity	100.0%;	Pred. No. 2.7e-123;		
Matches 432; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGGAGACCAATTTTCCCTCGACTCGAATTTAAATGTTATTATATCATTTATCACGTTGTTT	60
DB	33289	ATGGAGACCAATTTTCCCTCGACTCGAATTTAAATGTTATTATCATTTATCACGTTGTTT	33348
QY	61	GCCACAAGAATATTGCTTAAAGAATTTTATCTACTCCAAAAATGGTATCCCAGGAACA	120
DB	33349	GCCACAAGAATATTGCTTAAAGAATTTTATCTATCCAAAAATGGTATCCCGAACA	33408
QY	121	GTTGCTCAGCTAAGGATCTGATTTGGCCAAAAAGGAAGTGTTTGTTCCAGCAAGAATAC	180
DB	33409	GTTGCTCAGCTAAGGATCTGATTTGGCCAAAAAGGAAGTGTTTGTTCCAGCAAGAATAC	33468
QY	181	TGCCCTTACTGTAAGCTACTTTGTCTACCTCTTCCAAAGAAATTGAAAGTTCCTCCAAATCC	240
DB	33469	TGCCCTTACTGTAAGCTACTTTGTCTACCTCTTCCAAAGAAATTGAAAGTTCCTCCAAATCC	33528
QY	241	AGGGCCCTTGTTGGAAATTAGATGAAATGAGCAATGGCTCAGAGATTCAGAGACGCTTTA	300
DB	33529	AGGGCCCTTGTTGGAAATTAGATGAAATGAGCAATGGCTCAGAGATTCAGAGACGCTTTA	33588
QY	301	GAAGAAATCTCGGGCCAAAAAACTGTGACCTAAACGTATACATCAATGGCAAGCACATGGT	360
DB	33589	GAAGAAATCTCGGGCCAAAAAACTGTGACCTAAACGTATACATCAATGGCAAGCACATGGT	33648
QY	361	GGTAACAGCGAATTGGAAACTTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG	420
DB	33649	GGTAACAGCGAATTGGAAACTTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG	33708
QY	421	GTATTTCAATAG	432
DB	33709	GTATTTCAATAG	33720

RESULT 6	CR380957_05	WPCOMMENT	Sequence split into 13 fragments	LOCUS CR380957	Accession CR380957
			Fragment Name	Begin	End
			CR380957_00	1	110000
			CR380957_01	100001	210000
			CR380957_02	200001	310000
			CR380957_03	300001	410000
			CR380957_04	400001	510000

CR380957_05 500001 610000
CR380957_06 800001 710000
CR380957_07 700001 810000
CR380957_08 800001 910000
CR380957_09 900001 1010000
CR380957_10 1000001 1110000
CR380957_11 1100001 1210000
CR380957_12 1200001 1302002
Continuation 76 of 13) 500001 CR380957 from base 500001
Candida glabrata strain

Query Match	35.1%;	Score 151.6;	DB 4;	Length 110000;
Best Local Similarity	66.6%;	Pred. No. 4.8e-36;		
Matches 217;	Conservative 0;	Mismatches 109;	Indels 0;	Gaps 0;
Qy	100	AAATGGTATCCAGGAAACAGTGTCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTG	159	
Db	69321	AGATGGTAAAGCAAGACACTGTTAACTCCGTCAAGAACATGATCGGTCAAAAGAGATC	69380	
Qy	160	TTTGTGTGCAGCAAGACATPACTGCCCTTACTGTATAAGCTACTTTGTGTACCCCTCTTCCAA	219	
Db	69381	TTTGTGCGTCTCAAGAGTCTTACTTGCCCTTACTGTCAGAGCTGCTTAAGCAAAACCTGTTCGAA	69440	
Qy	220	GAATTGAAGCTTCCCAATCCCAAGGCCCTTGTGTGGAAATTAGATGAATGAGCAATGGC	279	
Db	69441	GAATTTGAAAGTCCCAATGACAAAGGCTGTGCTTCTAGAAATTTGGACGAAATTTGAAAGAGGT	69500	
Qy	280	TCAGAGATTCAGAGCGCTTTAGAAAGAAATCTCGGGCCAAAACCTGTACCTTAACGTATAC	339	
Db	69501	AGCGACATTTCAACAAGCTTTGCTGAAATCAACCGGTCAAAAACACTGTCCCAAAATATTTTAC	69560	
Qy	340	ATCAATGGCGAAGCACATTGGTGGTAACAGCGATTTGGAAAATCTTTGAAGAAAATATGGCAAG	399	
Db	69561	ATCATGGTCAACACATTGGTGGTAACAGTGACCTTACAAAATTAAGCAAAACCGGTAAA	69620	
Qy	400	TTAGCTGAAATATTGAAGCCGGTATT	425	
Db	69621	CTACAACCATTTGCTACAAAAGGTTTT	69646	

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RESULT 7
AX536464
LOCUS      833 bp      DNA
DEFINITION      Sequence 65 from Patent WO02064766.
ACCESSION      AX536464
VERSION      AX536464.1  GI:25262863
KEYWORDS
SOURCE      Saccharomyces cerevisiae (baker's yeast)
ORGANISM      Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1
Contreras,R.H., Eberhardt,I., Luyten,W.H. and Reekmans,R.J.
Bax-responsive genes for drug target identification in yeast and
fungi
Patent: WO 02064766-A 65 22-AUG-2002;
JANSSEN PHARMACEUTICA N.V. (BE)
Location/Qualifiers
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FEATURES
source
ORIGIN

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	Gaps	0			
Qy	99	AAAAATGGTATCCAGGAACAGTTGCTCACGTAAAGCATCTGATTGGCCAAAAAGGAAGT	158		
Db	497	AAAAATGGTATCTCAGAAACTATCAAGCAGCTCAAGGACCTTATTGCAGAAACGAGAT	556		
Qy	159	GTTTTGTGACGAAAGACATACCTGCCCTTACTGTAAAGCTACTTTGTCTACCTCTCTTCCA	218		

Db	557	CTTCGTGCATCCAAACGACTGTCCATACCTGCCATCGAGCCCTAAACACAGCGCTTTTGA	616	JOURNAL PUBMED AUTHORS	seven open reading frames including the RVS161, ADP1 and PGK genes
Qy	219	AGAATTGAAGCTTCCAAATCCAAAGCCCTTGTGTTGGAATTAGATGAATGAGCAATGG	278	REFERENCE	Yeast 8 (5), 409-417 (1992)
Db	617	AAAGTTAAAGGTTCCCAAGTCCAAAGTCTCTGGTTTGTGCAATTGAATGACATGAAGAAGG	676	REFERENCE	1626432
Qy	279	CTCAGAGATTCAGAGCGCTTTAGAAGAAATCTCGGCCCAAAACCTGTACCTTAACGTATA	338	TITLE	Oliver,S.G., van der Aart,Q.J., Agostoni-Carbone,M.L., Aigle,M.,
Db	677	CGCAGACATTCAGGCTGCGTTATATGAGATTAAATGGCCAAAGAACCGTGCCAAACATCTA	736	JOURNAL PUBMED AUTHORS	Alberghina,L., Alexandraki,D., Antoine,G., Anwar,R., Ballesta,J.P.,
Qy	339	CATCAATGGCAAGCACATTTGGTGTACAGCGATTTGGAACTTTGAAGAAAATGGCAA	398	REFERENCE	Benit,P. et al.
Db	737	TATTATGTTAAACATATTGGAGCGACGACGACTTGCAGGAATTGAGGAGACTGGTGA	796	TITLE	The complete DNA sequence of yeast chromosome III
Qy	399	GTTAGCTGAATATTGAAGCCGCTATTTCATA	431	JOURNAL PUBMED AUTHORS	Nature 357 (6373), 38-46 (1992)
Db	797	ATTGGAGGAATTGTTAGACCTATTCTTGCAA	829	REFERENCE	1574125
RESULT 8					
SCCHRII/c					
LOCUS	SCCHRIII	316613 bp	DNA linear	PLN 18-APR-2005	
DEFINITION	S.cerevisiae chromosome III complete DNA sequence.				
ACCESSION	X59720	S43845	S49180	S58064	S93798
VERSION	X59720.2	GI:14588895			
KEYWORDS	Chromosome.				
SOURCE	Saccharomyces cerevisiae (baker's yeast)				
ORGANISM	Saccharomyces cerevisiae				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
TITLE	Saccharomycetales; Saccharomycetaceae; Saccharomyces.				
JOURNAL	Rad,M.R., Lutzenkirchen,K., Xu,G., Kleinhaus,U. and Hollenberg,C.P.				
PUBMED	The complete sequence of a 11,953 bp fragment from C1G on				
AUTHORS	chromosome III encompasses four new open reading frames				
TITLE	Yeast 7 (5), 533-538 (1991)				
JOURNAL	1897318				
PUBMED					
AUTHORS	Biteau,N., Frenaux,C., Hebrard,S., Menara,A., Aigle,M. and				
TITLE	Crouzet,M.				
JOURNAL	The complete sequence of a 10.8kb fragment to the right of the				
PUBMED	chromosome III centromere of Saccharomyces cerevisiae				
AUTHORS	Yeast 8 (1), 61-70 (1992)				
TITLE	1580102				
JOURNAL	Wilson,C., Bergantino,E., Lanfranchi,G., Valle,G., Carignani,G. and				
PUBMED	Frontali,L.				
AUTHORS	A putative serine/threonine protein kinase gene on chromosome III				
TITLE	Of Saccharomyces cerevisiae				
JOURNAL	Yeast 8 (1), 71-77 (1992)				
PUBMED	1580103				
AUTHORS	Benit,P., Chanet,R., Fabre,F., Faye,G., Fukuhara,H. and Sor,F.				
TITLE	Sequence of the sup61-RAD18 region on chromosome III of				
JOURNAL	Saccharomyces cerevisiae				
PUBMED	Yeast 8 (2), 147-153 (1992)				
AUTHORS	1561837				
TITLE	Bolle,P.A., Gilliquet,V., Berben,G., Dumont,J. and Hilger,F.				
JOURNAL	The complete sequence of K3B, a 7.9 kb fragment between PGK1 and				
PUBMED	CRY1 on chromosome III, reveals the presence of seven open reading				
AUTHORS	frames				
TITLE	Yeast 8 (3), 205-213 (1992)				
JOURNAL	1574926				
PUBMED					
AUTHORS	Sor,F., Cheret,G., Fabre,F., Faye,G. and Fukuhara,H.				
TITLE	Sequence of the HWR region on chromosome III of Saccharomyces				
JOURNAL	cerevisiae				
PUBMED	Yeast 8 (3), 215-222 (1992)				
AUTHORS	1574927				
TITLE	Skala,J., Purnelle,B. and Goffeau,A.				
JOURNAL	The complete sequence of a 10.8 kb segment distal of SUP2 on the				
PUBMED	right arm of chromosome III from Saccharomyces cerevisiae reveals				
AUTHORS					
TITLE					

JOURNAL PUBMED AUTHORS	seven open reading frames including the RVS161, ADP1 and PGK genes
REFERENCE	Yeast 8 (5), 409-417 (1992)
TITLE	1626432
JOURNAL PUBMED AUTHORS	Oliver,S.G., van der Aart,Q.J., Agostoni-Carbone,M.L., Aigle,M.,
REFERENCE	Alberghina,L., Alexandraki,D., Antoine,G., Anwar,R., Ballesta,J.P.,
TITLE	Benit,P. et al.
JOURNAL PUBMED AUTHORS	The complete DNA sequence of yeast chromosome III
REFERENCE	Nature 357 (6373), 38-46 (1992)
TITLE	1574125
JOURNAL PUBMED AUTHORS	Wilson,C., Grisanti,P. and Frontali,L.
REFERENCE	The complete sequence of a 6146 bp fragment of Saccharomyces
TITLE	cerevisiae chromosome III contains two new open reading frames
JOURNAL PUBMED AUTHORS	Yeast 8 (7), 569-575 (1992)
REFERENCE	1523889
TITLE	Scherens,B., Messenguy,F., Gigot,D. and Dubois,E.
JOURNAL PUBMED AUTHORS	The complete sequence of a 9,543 bp segment on the left arm of
REFERENCE	chromosome III reveals five open reading frames including
TITLE	glucokinase and the protein disulfide isomerase
JOURNAL PUBMED AUTHORS	Yeast 8 (7), 577-585 (1992)
REFERENCE	1523890
TITLE	Defoor,S., Debrabandere,R., Keyers,B., Voet,M. and Volckaert,G.
JOURNAL PUBMED AUTHORS	Nucleotide sequence of D10B, a BamHI fragment on the small-ring
REFERENCE	chromosome III of Saccharomyces cerevisiae
TITLE	Yeast 8 (8), 681-687 (1992)
JOURNAL PUBMED AUTHORS	1441748
REFERENCE	12 (bases 169581 to 171116; 171683 to 172169)
TITLE	Agostoni Carbone,M.L., Panzeri,L., Muzi Falconi,M., Carcano,C.,
JOURNAL PUBMED AUTHORS	Plevani,P. and Lucchini,G.
REFERENCE	Nucleotide sequence of 9.2 kb left of CRY1 on yeast chromosome III
TITLE	from strain AB972: evidence for a Ty insertion and functional
JOURNAL PUBMED AUTHORS	analysis of open reading frame YCR28
REFERENCE	Yeast 8 (9), 805-812 (1992)
TITLE	1332309
JOURNAL PUBMED AUTHORS	13 (bases 1 to 315338)
REFERENCE	TA-repeat microsatellites are closely associated with ARS consensus
TITLE	sequences in yeast chromosome III
JOURNAL PUBMED AUTHORS	Yeast 9 (7), 753-759 (1993)
REFERENCE	8368009
TITLE	14 (bases 1 to 315338)
JOURNAL PUBMED AUTHORS	Slonimski,P.P. and Brouillet,S.
REFERENCE	A data-base of chromosome III of Saccharomyces cerevisiae
TITLE	Yeast 9 (9), 941-1029 (1993)
JOURNAL PUBMED AUTHORS	8266725
REFERENCE	15 (bases 1 to 315339)
TITLE	Rodriguez-Cousino,N., Lill,R., Neupert,W. and Court,D.A.
JOURNAL PUBMED AUTHORS	Identification and initial characterization of the cytosolic
REFERENCE	protein Ycr77p
TITLE	Yeast 11 (6), 581-585 (1995)
JOURNAL PUBMED AUTHORS	7645349
REFERENCE	16
TITLE	MIPS.
JOURNAL PUBMED AUTHORS	Direct Submission
REFERENCE	Submitted (16-MAR-1992) MIPS, D-8033 Martinsried, FRG. Data
TITLE	collected by MIPS on behalf of the European Yeast Chromosome III
JOURNAL PUBMED AUTHORS	Sequencing project
REFERENCE	replaced by [13]
TITLE	17 (bases 1 to 314957)
JOURNAL PUBMED AUTHORS	Jimenez,A.
REFERENCE	Direct Submission
TITLE	Submitted (28-DEC-1992) MIPS, D-8033 Martinsried, FRG. Data
JOURNAL PUBMED AUTHORS	collected by MIPS on behalf of the European Yeast Chromosome III
REFERENCE	Sequencing project. Update originating from A. Jimenez
TITLE	replaced by [14]
JOURNAL PUBMED AUTHORS	18
REFERENCE	Louis,E.J.
TITLE	Direct Submission
JOURNAL PUBMED AUTHORS	Submitted (25-JUN-1993) MIPS, D-8033 Martinsried, FRG. Data
REFERENCE	collected by MIPS on behalf of the European Yeast Chromosome III

angueta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source Location/Qualifiers

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Best Local Similarity 86.6%; Pred. No. 2.4e-34;
Matches 162; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 246 CTTGTGTTGGAATTAGTGAATGAGCAATGCTCAGAGATTCAGAGCGCTTTAGAAGA 305
DB 1 CGTTGTTTGGATTGGACGAATGAGCAATGCTTCAGAAATTCAGAGATGCTCTCGAAGA 60
QY 306 AATCTCGGGCCAAAACACTGTACTACGTATACATCAATGGCAACGATGGTGCTGATAA 365
DB 61 AATTTTCGGCCGAGAAACCGTACCAACGGTTTATATCAATGGAAACACATCGTGATAA 120
QY 366 CAGCGATTGGAACTTTGAAGAAAATGCGAAGTTAGCTGTAATATTGAAGCGCGTATT 425
DB 121 CAGCGATTGGAGCTTTGAAGAAAACGTAAGTTGGCTGTAATATTGAAGCGCGTATT 180
QY 426 TCAATAG 432
DB 181 TGAATAG 187

RESULT 10

CQ785688
LOCUS CQ785688 333 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 1 from Patent WO2004018687.
ACCESSION CQ785688
VERSION CQ785688.1 GI:45720868
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1
AUTHORS Chardonens,A. and Puzio,P.
TITLE Nucleic acid sequences encoding proteins associated with abiotic stress response
JOURNAL Patent: WO 2004018687-A 1 04-MAR-2004;
BASF Plant Science GmbH (DE)

FEATURES

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ORIGIN

Query Match 33.2%; Score 143.4; DB 2; Length 333;
Best Local Similarity 64.7%; Pred. No. 3.7e-33;
Matches 213; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 103 ATGGTATCCAGGAAACAGTTGCTCAGTAAAGGATCTGATGGCCAAAGAAAGTGTTT 162
DB 1 ATGGTATCTCAAGAAACTATCAAGCAGCTCAAGGACCTTATTGCGAAGAACGATCTTC 60
QY 163 GTTGCGAGCAACACATACCTGCCCCTTACTGTAAAGCTACTTTCTCTACCTCTTCCAGAA 222
DB 61 GTCGCATCCAAACGCTACTGTCATCTGCCATGCCCTAAACACGCTTTTGAAGAG 120
QY 223 TTGAACGTTCCCAATCCAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGCTCA 282
DB 121 TTAAGAGTTCCAGGTCCTCAAGAGTTCTGGTTTGCATTTGAATGACATGAAGGAGCGCA 180
QY 283 GAGATTCAAGACGCTTTTGAAGAAATCTCGGGCCCAAAAACCTGTACTAACGTATACATC 342
DB 181 GACATTCAGGCTGCGTTATATGAGATTAAATGCGCAAGAACCGTGCCAAACATCTATAT 240
QY 343 AATGCAAGCACATTTGGTGTAAACAGCGATTTGGAAACTTTGAAGAAAATGGCAAGTTA 402
DB 241 AATGTTAAACATATTGGAGGCAACGACGACTTTGCAGGAATTCAGGAGACTGCTGTAATTG 300
QY 403 GCTGAATATTGAAGCGCGTATTTCATA 431
DB 301 GAGGAATTGTTAGAACCTATTCTTGCAAA 329

RESULT 11

CR382123_00/c

WPCOMMENT

Sequence split into 18 fragments LOCUS CR382123 Accession CR382123

Fragment Name	Begin	End
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CR382123_02	200001	310000
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CR382123_09	900001	1010000
CR382123_10	1000001	1110000
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CR382123_15	1500001	1610000
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CR382123_17	1700001	1753957

LOCUS

CR382123 1753957 bp DNA linear PLN 17-APR-2005

DEFINITION Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-1140 of Kluyveromyces lactis.

ACCESSION CR382123

VERSION CR382123.1 GI:49641331

KEYWORDS genomic DNA.

SOURCE Kluyveromyces lactis NRRL Y-1140

ORGANISM

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
REFERENCE 1 (bases 1 to 1753957)
AUTHORS Dujon,B., Sherman,D., Fischer,G., Durrens,P., Casaregola,S., Lafontaine,I., De Montigny,J., Marck,C., Neuveglise,C., Talla,E., Goffard,N., Frangeul,L., Aigle,M., Anthouard,V., Babour,A.,

Barbe, V., Barnay, S., Blanchin, S., Beckerich, J. M., Beyne, E., Bleykaster, C., Boisarane, A., Boyer, J., Cattolico, L., Confanioli, F., De Daruvar, A., Despons, L., Fabre, E., Fairhead, C., Ferry-Dumazet, H., Groppi, A., Hantraye, F., Hennequin, C., Jauniaux, N., Joyet, P., Kachouri, R., Kerrest, A., Koszul, R., Lemaire, M., Lesur, I., Ma, L., Muller, H., Nicaud, J. M., Nikolski, M., Oztas, S., Ozier-Kalogeropoulos, O., Pellenz, S., Potier, S., Richard, G. F., Straub, M. L., Suleau, A., Swennen, D., Tekala, F., Wesolowski-Louvel, M., Westhof, E., Wirth, B., Zeniou-Meyer, M., Zivanovic, I., Bolotin-Fukuhara, M., Thierry, A., Bouchier, C., Caudron, B., Scarpelli, C., Gaillardin, C., Weissenbach, J., Wincker, P. and Souciet, J. L.

Genolevures
Genome evolution in yeasts
NATURE 430 (6995), 35-44 (2004)
PUBMED 15229592
REFERENCE 2 (bases 1 to 1753957)
GENOSCOPE
Direct Submission
Submitted (01-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex -FRANCE (E-mail : secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Finished sequence obtained at Genoscope. Annotations made by the Genolevures Consortium.
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CUS   15961..16272
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Query Match Best Local Similarity 63.1%; Pred. No. 1.1e-31;
Matches 212; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
QY 89 TATCTACTCCAAAATGGTATCCAGGAACACATCTGCTCACGTAAAGGATCGATTGGCC 148
Db 102013 TACATCTTTCAAAAATGCCAAGTGCAGCAACAATCGTCTGTCCTCAAGGTTTAATCAACT 101954
QY 149 AAAAGGAAGTGTGTGTGACGACAAAGACATCTGCTCAAGTAAAGCTTCTGTCTA 208
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QY 209 CCTCTTCCAAAGATTGAAGCTTCCCAATCCAGGCCCTTGTGTGGAAATAGATGAAA 268
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Db 101833 TAGAAGATGGTTCGGATATTCAGGATGCTTTGGCAGAAATACCGGCCAAAGACTGTTTC 101774
QY 329 CTAACTGTATACATCAATGGCAAGCATTGGTGGTAAACAGCATTGGGAAACTTTGAAGA 388
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CR382123_02 200001 310000
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CR382123_15 1500001 1610000
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, Continuation (2 of 18) of CR382123 from base 100001 (CR382123 Kluyveromyces lactis strai
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Query Match 31.9%; Score 137.6; DB 4; Length 110000;
Best Local Similarity 63.1%; Pred. No. 1.1e-31;
Matches 212; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
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QY 149 AAAAGGAAGTGTGTGTGACGACAAAGACATCTGCTCAAGCTTCTGTGTAAAGTACTTTGTCTA 208
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QY 209 CCTCTTCCAAAGATTGAAGCTTCCCAATCCAGGCCCTTGTGTGGAAATAGATGAAA 268
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Db 1833 TAGAAGATGGTTCGGATATTCAGGATGCTTTGGCAGAAATACCGGCCAAAGACTGTTTC 1774
QY 329 CTAACTGTATACATCAATGGCAAGCATTGGTGGTAAACAGCATTGGGAAACTTTGAAGA 388
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Db 1713 ACTCCGGTATTTGGATAAGTTGTGCTTCCTTAT 1678

RESULT 13
AX489480
LOCUS AX489480
DEFINITION Sequence 6780 from Patent WO02053728.
ACCESSION AX489480
VERSION AX489480.1 GI:23233492
KEYWORDS Candida albicans
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitospotic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Roemer T., Jiang B., Boone C., Bussey H. and Ohlsen, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 6780 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
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/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

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Best Local Similarity 55.4%; Pred. No. 3.2e-16;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;
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QY 127 CAGCTAAAGATCTGATGGCCAAAAGGAGTGTGTGTGACGACAAAGACATACATCGCCT 186
Db 70 AAGGTCGAACAATTGATCAAAACCAACACAGTTTTCATTGCTCCAAATCCCTATTGTCCA 129
QY 187 TACTGTAAAGTACTTTTGTCTACCTCTTCCCAAGAAATGAACGTTCCCAAAATCCAAAGGCC 246
Db 130 TACTGTAAAGGCTACCAAGACAC-----AATTGAAGCTATACAAAGGATGCT 177
QY 247 CTTGTGTTGGAATTAGATGAATAGCAATGCGTCTCAGAGATTCAAGACCTTTTAGAAGAA 306
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Qy 307 ATCTCGGCCCAAAAACCTGACCTTAACGTATACATCAATGCGAAGCAATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAAATGTCTTTATTGGTGTCAACATATTGGTGGCAAT 297
Qy 367 AGCGATTGGAACTTTGAGAAAAATGCGAAGTACTGAAATATTGAAGCCGGTATTT 426
Db 298 TCCGATGTGAAGCTTTGAAGTCTAGTGACAAATTAGATGACAAATCAAAGCTGCTTTA 357
Qy 427 CAA 429
Db 358 TAA 360
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AX537006
LOCUS AX537006 360 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 607 from Patent WO02064766.
ACCESSION AX537006
VERSION AX537006.1 GI:25263441
KEYWORDS
SOURCE
ORGANISM Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Contreras,R.H., Eberhardt,I., Luyten,W.H. and Reekmans,R.J.
TITLE Bax-responsive genes for drug target identification in yeast and
fungi
JOURNAL Patent: WO 02064766-A 607 22-AUG-2002;
JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES
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Location/Qualifiers
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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Query Match 20.6%; Score 89; DB 2; Length 360;
Best Local Similarity 55.4%; Pred. No. 3.2e-16;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;
Qy 67 AGAATTATGCTAAAGATTTTATCTACTCCAAAAATGGTATCCAGGAAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC 69
Qy 127 CAGTAAAGGATCTGATGGCCAAAGCAAGTGTGTTGTCAGCAAGACATACTGCCCT 186
Db 70 AAGGTGCAACAATTGATCAAAACCAACCAAGTGTTCATTGCTCCAAATCCTATTGTCCA 129
Qy 187 TACTGTAAAGTACTTTGTCTACCCCTCTTCCAAGAAATTGAACGTTCCCAAAATCCAAGGCC 246
Db 130 TACTGTAAAGCTACCAAAAGCAC-----AATTGAAGCTATAACAAGGATGCT 177
Qy 247 CTTGTGTGGAATPAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAA 306
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Qy 307 ATCTCGGCCCAAAAACCTGACCTTAACGTATACATCAATGCGAAGCAATTTGGTGTAAAC 366
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Qy 367 AGCGATTGGAACTTTGAGAAAAATGCGAAGTACTGAAATATTGAAGCCGGTATTT 426
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Qy 427 CAA 429
Db 358 TAA 360

RESULT 15
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WPCOMMENT

Sequence split into 33 fragments LOCUS CR382129 Accession CR382129
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Query Match 19.4%; Score 83.8; DB 4; Length 110000;
Best Local Similarity 55.0%; Pred. No. 6e-15;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 1;
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Db 95727 GACGTTTCTTCTACAAACCATGGCCACCGAGTCCGCTATCAAGACCATCAAGGAGCACA 95668
Qy 143 TTGGCCAAAGGAAGTGTGTTGTCAGCAAGACATACCTGCCCTTACTGTAAAGCTACTT 202
Db 95667 TTGCCAAGGACAAAGGTCTTCGTGGCCCTCCAAAGTCTTACTGCCCTTACTGCAAGCAGCA 95608
Qy 203 TGTCTACCCCTTCTCCAAAGAATTGAACGTTCCCAAAATCCCAAGGCCCTTGTGTTGGAATTAG 262
Db 95607 AGCAGCTGTCTTCCCAAGTTCAAGGAGG-----CCAAGCCGCGTATTCTCGAGCTCG 95557
Qy 263 ATGAAATGAGCAATGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGGGCCAAAAA 322
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Qy 323 CTGTACTTAACGTATACATCAATGGCAAGCACATTTGGTGTAAACGATTTTGGAACTT 382
Db 95496 CCGTTCCTCAACGTTTTCATTTGGAGGGCCAGCACATTTGGTGCAACTCCGATCTCGAGGTT 95437
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Search completed: November 7, 2006, 04:29:46
Job time : 3046 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2006, 19:18:05 ; Search time 187 Seconds
(without alignments)
354.223 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDNLIVIIITL.....DLTLKKNGKLAEILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /EMC_Celerra_SID83/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /EMC_Celerra_SID83/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 3: /EMC_Celerra_SID83/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
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- 5: /EMC_Celerra_SID83/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /EMC_Celerra_SID83/ptodata/2/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	4	US-10-451-467A-134
2	714	100.0	143	5	US-10-523-362-4
3	391	54.8	110	4	US-10-451-467A-66
4	391	54.8	110	5	US-10-523-362-2
5	300.5	42.1	119	4	US-10-032-585-7780
6	300.5	42.1	119	4	US-10-451-467A-608
7	230.5	32.0	135	4	US-10-767-701-42668
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9	228.5	32.0	135	4	US-10-425-115-229409
10	225	31.5	104	4	US-10-425-115-362857
11	219	30.7	101	4	US-10-767-701-51857
12	218.5	30.6	131	6	US-11-096-568A-26784
13	216.5	30.3	129	4	US-10-425-115-352583
14	216.5	30.3	129	4	US-10-425-115-229411
15	216	30.3	136	4	US-10-424-599-239954
16	216	30.3	136	4	US-10-437-963-149594
17	215.5	30.2	136	5	US-10-523-362-46
18	215	30.1	102	4	US-10-523-362-48
19	215	30.1	113	6	US-11-096-568A-26785
20	215	30.1	135	5	US-10-523-362-32
21	214.5	30.0	133	5	US-10-523-362-22
22	211.5	29.6	134	4	US-10-424-599-239952
23	209	29.3	112	4	US-10-437-963-131826
24	208	29.1	134	4	US-10-424-599-239955
25	207.5	29.1	173	5	US-10-523-362-20
26	206	28.9	102	4	US-10-425-115-331215
27	206	28.9	111	5	US-10-523-362-28

28	205.5	28.8	128	4	US-10-767-701-43209	Sequence 43209, A
29	205	28.7	97	4	US-10-425-115-312491	Sequence 312491, A
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31	204	28.6	120	5	US-10-523-362-16	Sequence 16, Appl
32	199	27.9	129	4	US-10-424-599-175134	Sequence 175134, A
33	199	27.9	179	5	US-10-523-362-34	Sequence 34, Appl
34	198	27.7	111	5	US-10-523-362-26	Sequence 26, Appl
35	197	27.6	136	5	US-10-523-362-18	Sequence 18, Appl
36	196.5	27.5	116	6	US-11-097-143-17640	Sequence 17640, A
37	196	27.5	130	5	US-10-523-362-30	Sequence 30, Appl
38	194	27.2	127	4	US-10-451-467A-598	Sequence 598, App
39	189	26.5	114	6	US-11-097-143-15012	Sequence 15012, A
40	185.5	26.0	131	4	US-10-437-963-154842	Sequence 154842, A
41	184.5	25.8	166	4	US-10-424-599-159065	Sequence 159065, A
42	184.5	25.8	177	4	US-10-425-115-201600	Sequence 201600, A
43	184	25.8	164	4	US-10-424-599-175133	Sequence 175133, A
44	183	25.6	105	4	US-10-425-115-308251	Sequence 308251, A
45	181	25.4	107	4	US-10-424-599-146193	Sequence 146193, A

ALIGNMENTS

RESULT 1

US-10-451-467A-134

; Sequence 134, Application US/10451467A

; Publication No. US20040161840A1

; GENERAL INFORMATION:

; APPLICANT: CONTRERAS, ROLAND HENRI

; APPLICANT: EBERHARDT, INES

; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS

; APPLICANT: REEKMAN, RIEKA JOSEPHINA

; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN

; TITLE OF INVENTION: YEAST AND FUNGI

; FILE REFERENCE: JAB-1667

; CURRENT APPLICATION NUMBER: US/10/451,467A

; CURRENT FILING DATE: 2003-06-19

; PRIOR APPLICATION NUMBER: EP 00870318.3

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: EP 01870002.1

; PRIOR FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: EP 01870003.9

; PRIOR FILING DATE: 2001-01-09

; NUMBER OF SEQ ID NOS: 732

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 134

; LENGTH: 143

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-451-467A-134

Query Match 100.0%; Score 714; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.7e-69;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	METNFSFDNLIVIIITL	FATRIIAKRLFLSPKMWQETVAHVKDLIGQKEVFVAAKTY	60
DB	1	METNFSFDNLIVIIITL	FATRIIAKRLFLSPKMWQETVAHVKDLIGQKEVFVAAKTY	60
QY	61	CPYCKATLSTL	FQELNVPKSKALVLELDENSGSETQDALEETISGQKTPNVNINKGHIG	120
DB	61	CPYCKATLSTL	FQELNVPKSKALVLELDENSGSETQDALEETISGQKTPNVNINKGHIG	120

QY 121 GNSDLETLKKNGKLAEILKPVFQ 143

DB 121 GNSDLETLKKNGKLAEILKPVFQ 143

RESULT 2

US-10-523-362-4

; Sequence 4, Application US/10523362

; Publication No. US20060064784A1

; GENERAL INFORMATION:

APPLICANT: Chardonens, Agnes
APPLICANT: Puzio, Piotr
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
FILE REFERENCE: 532622010300
CURRENT FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 143
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-523-362-4

Query Match 100.0%; Score 714; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.7e-69;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 METNFSFDSNLIVIIITLPTATRIIAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTY 60
QY 61 CPYCKATLSTLFOELNVPKSKALVLELDMSGSEIQDALEEEISGQKTPNVNVIKNGHIG 120
Db 61 CPYCKATLSTLFOELNVPKSKALVLELDMSGSEIQDALEEEISGQKTPNVNVIKNGHIG 120
QY 121 GNSDLETLLKNGKLAELIKPVFQ 143
Db 121 GNSDLETLLKNGKLAELIKPVFQ 143

RESULT 3

US-10-451-467A-66
Sequence 66, Application US/10451467A
Publication No. US20040161840A1
GENERAL INFORMATION:
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMAN, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 110
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-66

Query Match 54.8%; Score 391; DB 4; Length 110;
Best Local Similarity 64.5%; Pred. No. 4.9e-34;
Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

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Db 1 MVSQETIKHVKDLIAENEIFVASKTYCPYCHAAALNTLFEKLVPRSKVLVLQNDMKEGA 60
QY 95 EIQDALEEEISGQKTPNVNVIKNGHIGNSDLETLLKNGKLAELIKPV 141
Db 61 DIQAALYEINGQRTVPNVNVIKNGHIGNSDLETLLKNGKLAELIKPV 107

RESULT 4

US-10-523-362-2
Sequence 2, Application US/10523362
Publication No. US20060064784A1
GENERAL INFORMATION:
APPLICANT: Chardonens, Agnes
APPLICANT: Puzio, Piotr
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
FILE REFERENCE: 532622010300
CURRENT FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 110
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-523-362-2

Query Match 54.8%; Score 391; DB 5; Length 110;
Best Local Similarity 64.5%; Pred. No. 4.9e-34;
Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 35 MVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDMSG 94
Db 1 MVSQETIKHVKDLIAENEIFVASKTYCPYCHAAALNTLFEKLVPRSKVLVLQNDMKEGA 60
QY 95 EIQDALEEEISGQKTPNVNVIKNGHIGNSDLETLLKNGKLAELIKPV 141
Db 61 DIQAALYEINGQRTVPNVNVIKNGHIGNSDLETLLKNGKLAELIKPV 107

RESULT 5

US-10-032-585-7780
Sequence 7780, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10192-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7780
LENGTH: 119
TYPE: PRT
ORGANISM: Candida albicans
US-10-032-585-7780

Query Match 42.1%; Score 300.5; DB 4; Length 119;
Best Local Similarity 50.4%; Pred. No. 3.2e-24;
Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;

QY 19 LPATRIIAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVP 78
Db 1 MERT-LLTGRLTNTSTMVSSQVKNKVEQLIKTPVFIASKSYCPYCKATKST---IEAI 55
QY 79 KSKALVLELDMSGSEIQDALEEEISGQKTPNVNVIKNGHIGNSDLETLLKNGKLAEL 138
Db 56 TKDAVILELDEVDGAEIQEALLETGQRTVPNVNVIKNGHIGNSDLETLLKNGKLAEL 115
QY 139 K 139
Db 116 K 116

RESULT 6

US-10-451-467A-608

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:12:20 ; Search time 41 Seconds
(without alignments)

335.585 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDSNLIVIIITLF.....DLETLKNGKLAILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	1 GDBY	glutaredoxin - yea
2	391	54.8	110	1 S19363	glutaredoxin GRX1
3	224	31.4	109	2 T48748	probable glutaredoxin
4	212	29.7	101	2 T38824	thioltransferase -
5	209	29.3	112	2 JC5445	glutaredoxin - ric
6	203	28.4	102	2 S54825	glutaredoxin - cas
7	199	27.9	179	2 B84587	probable glutaredoxin
8	196	27.5	130	2 G96802	probable glutaredoxin
9	194	27.2	134	2 T12219	glutaredoxin I - c
10	178	24.9	110	2 T37724	probable thioltran
11	154	21.6	149	2 T16026	hypothetical prote
12	151.5	21.2	105	1 GDPG	glutaredoxin - pig
13	151.5	21.2	203	1 S45869	glutaredoxin homol
14	147.5	20.7	105	1 GDBO	glutaredoxin - bov
15	146	20.4	102	2 B71422	probable glutaredoxin
16	143	20.0	106	1 S47472	glutaredoxin - hum
17	143	20.0	231	1 S52509	probable membrane
18	142	19.9	176	2 T04526	hypothetical prote
19	141.5	19.8	106	1 GDRB	glutaredoxin - rab
20	140	19.6	102	2 H71421	probable glutaredoxin
21	136	19.0	102	2 F71421	probable glutaredoxin
22	136	19.0	102	2 A71422	probable glutaredoxin
23	136	19.0	102	2 G71421	probable glutaredoxin
24	136	19.0	102	2 H86160	hypothetical prote
25	131	18.3	102	2 T48082	glutaredoxin-like
26	125.5	17.6	92	2 AC3275	glutaredoxin [impo
27	124.5	17.4	103	2 T48084	glutaredoxin-like
28	124.5	17.4	108	1 E42510	glutaredoxin 1 - v
29	124	17.4	107	2 AE1906	hypothetical prote

ALIGNMENTS

RESULT 1

GDBY

Glutaredoxin - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YDR513w; thioltransferase

C;Species: Saccharomyces cerevisiae

C;Date: 31-Dec-1990 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S69570; JQ1612; A35492

R;Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A;Description: The sequence of S. cerevisiae cosmid 8166, 9787, 9717, and lambda 3073.

A;Reference number: S69553

A;Accession: S69570

A;Molecule type: DNA

A;Residues: 1-143 <DIE>

A;Cross-references: UNIPROT:P17695; UNIPARC:UPI000004F902; EMBL:U33057; NID:g927764; PID:

R;Gan, Z.R.

Biochem. Biophys. Res. Commun. 187, 949-955, 1992

A;Title: Cloning and sequencing of a gene encoding yeast thioltransferase.

A;Reference number: JQ1612; MUID:92412147; PMID:1530649

A;Accession: JQ1612

A;Molecule type: DNA

A;Residues: 35-143 <GAN>

A;Cross-references: UNIPARC:UPI0000168989; GB:S45268; NID:g256162; PIDN:AAB23389.1; PID:

R;Gan, Z.R.; Polokoff, M.A.; Jacobs, J.W.; Sardana, M.K.

Biochem. Biophys. Res. Commun. 188, 944-951, 1990

A;Title: Complete amino acid sequence of yeast thioltransferase (glutaredoxin).

A;Reference number: A35492; MUID:90267489; PMID:2189409

A;Accession: A35492

A;Molecule type: protein

A;Residues: 36-141 <GA2>

A;Cross-references: UNIPARC:UPI0000171E32

C;Genetics:

A;Gene: SGD:TTR1; GRX2; MIPS:YDR513W

A;Cross-references: SGD:S0002921; MIPS:YDR513W

A;Map position: 4R

C;Function:

A;Description: thioltransferase catalyzes cellular thiol-disulfide transhydrogenation re

C;Superfamily: glutaredoxin; glutaredoxin homology

C;Keywords: acetylated amino end; cytosol; electron transfer; redox-active disulfide

F;36-141/Product: glutaredoxin #status experimental <MAT>

F;43-138/Domain: glutaredoxin homology <GLUT>

F;36/Modified site: acetylated amino end (Val) (in mature form) #status experimental

F;61-64/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 714; DB 1; Length 143;

Best Local Similarity 100.0%; Pred. No. 6.8e-56;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METNFSFDSNLIVIIITLFPATRIIAKFLSTPKQVSTQETVAHVKDLIGQKEVFVAQTY 60

Db 1 METNFSFDSNLIVIIITLFPATRIIAKFLSTPKQVSTQETVAHVKDLIGQKEVFVAQTY 60

QY 61 CPYCKATLSTLFQELNVPKSKALVLELDMSGSEIQTDALEEEISGQKTVPNVYINGKHIG 120
 DB 61 CPYCKATLSTLFQELNVPKSKALVLELDMSGSEIQTDALEEEISGQKTVPNVYINGKHIG 120
 QY 121 GNSDLETLLKNGKLAELIKPVFQ 143
 DB 121 GNSDLETLLKNGKLAELIKPVFQ 143

RESULT 2

S19363
 N;Alternate names: glutaredoxin GRX1 - yeast (Saccharomyces cerevisiae)
 C;Species: Saccharomyces cerevisiae
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: S19363
 R;Hollenberg, C.P.; Kleinhaus, U.; Lutzenkirchen, K.; Ramezani Rad, M.; Xu, G.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: S19350
 A;Accession: S19363
 A;Molecule type: DNA
 A;Residues: 1-110 <HOL>
 A;Cross-references: UNIPROT:P25373; UNIPARC:UPI000004F8E0; EMBL:X59720; NID:g19071116; P1
 C;Genetics:
 A;Gene: GRX1
 A;Cross-references: SGD:S0000540; MIPS:YCL035C
 A;Map position: 3L
 C;Function:
 A;Description: thioltransferase catalyzes cellular thiol-disulfide transhydrogenation re
 C;Superfamily: glutaredoxin; glutaredoxin homology
 C;Keywords: electron transfer; redox-active disulfide
 F;9-104/Domain: glutaredoxin homology <GLUT>
 F;27-30/Disulfide bonds: redox-active #status predicted

Query Match 54.8%; Score 391; DB 1; Length 110;
 Best Local Similarity 64.5%; Pred. No. 1.5e-27;
 Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 35 MVSQETVAHVKDLIGQKEVFVAARTYCPYCKATLSTLFQELNVPKSKALVLELDMSGSE 94

DB 1 MVSQETIKHVKDLIAENEIVASKTYCPYCHAAALNTLFEKLKVPKSKVLVLQNDMKEGA 60

QY 95 EIQDALEEEISGQKTVPNVYINGKHIGNSDLETLLKNGKLAELIKPV 141

DB 61 DIQAALYEINGQRTVPNVYINGKHIGGNDLQELRETGELELELEPI 107

RESULT 3

T48748
 probable glutaredoxin 8D4.220 [similarity] - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: T48748
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z24541
 A;Accession: T48748
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-109 <SCH>

A;Cross-references: UNIPROT:Q99718; UNIPARC:UPI000006A1A0; EMBL:AL353819; GSPDB:GN00112;
 A;Experimental source: cosmid contig 8D4; strain 74
 C;Genetics:
 A;Gene: NCSP:8D4.220
 A;Map position: 2
 A;Introns: 19/1

C;Superfamily: glutaredoxin; glutaredoxin homology
 C;Keywords: electron transfer; redox-active disulfide
 F;26-29/Disulfide bonds: redox-active #status predicted

Query Match 31.4%; Score 224; DB 2; Length 109;
 Best Local Similarity 42.6%; Pred. No. 8.2e-13;

Matches 46; Conservative 22; Mismatches 36; Indels 4; Gaps 1;
 QY 36 VSOETVAHVKDLIGQKEVFVAARTYCPYCKATLSTLFQELNVPKSKALVLELDMSGSE 95
 DB 1 MSDAATQAKQKQINDNAVVFVFSKYCPYCSNTK- - - QILDGUNAAYATYELNQESDGS 56
 QY 96 IODALEEEISGQKTVPNVYINGKHIGNSDLETLLKNGKLAELIKPVFQ 143
 DB 57 VQDALLKLTGQRTVPNVIFGIQKHIGNSDLEAVVKNKNGKGIQELLQ 104

RESULT 4

T38824

thioltransferase - fission yeast (Schizosaccharomyces pombe)

N;Alternate names: glutaredoxin

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T38824; T43362; T50489

R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21813

A;Accession: T38824

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-101 <CON>

A;Cross-references: UNIPROT:O36032; UNIPARC:UPI000012B7C0; EMBL:Z98980; PIDN:CAB11722.1;

A;Experimental source: strain 972h(-); cosmid c4F10

R;Kawamukai, M.

submitted to the EMBL Data Library, June 1998

A;Description: S.pombe glutaredoxin.

A;Reference number: Z22451

A;Accession: T43362

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-101 <KAW>

A;Cross-references: UNIPARC:UPI000012B7C0; EMBL:AB015167; PIDN:BAA28750.1

R;Kim, H.G.; Cho, Y.W.; Park, E.H.; Lim, C.J.

submitted to the EMBL Data Library, January 1999

A;Description: Characterization of cDNA encoding thioltransferase (glutaredoxin) from Sci

A;Reference number: Z25091

A;Accession: T50489

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-101 <KIM>

A;Cross-references: UNIPARC:UPI000012B7C0; EMBL:AF121275; PIDN:AAD25391.1

C;Genetics:

A;Gene: grx1; SPAC4F10.20

A;Map position: 1

A;Introns: 7/3; 25/2; 58/1

C;Superfamily: glutaredoxin; glutaredoxin homology

C;Keywords: electron transfer; redox-active disulfide

F;25-28/Disulfide bonds: redox-active #status predicted

Query Match 29.7%; Score 212; DB 2; Length 101;

Best Local Similarity 46.2%; Pred. No. 8.6e-12;

Matches 42; Conservative 17; Mismatches 28; Indels 4; Gaps 1;

QY 44 VKDLIGQKEVFVAARTYCPYCKATLSTLFQELNVPKSKALVLELDMSGSEIQTDALEEI 103

DB 8 VDSAVADNDVVVFAKSYCPYCHATEKVIADK- - - KIKAAQVYQIDLMNNGDEIQSYLLKK 63

QY 104 SQQKTVPNVYINGKHIGNSDLETLLKNGKL 134

DB 64 TQQRTPNVNIFHQKHVGGNSDFQALFKKGE 94

RESULT 5

JC5445

glutaredoxin - rice

N;Alternate names: thioltransferase

C;Species: Oryza sativa (rice)

C;Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C;Accession: JC5445; PC4325; S41736

R;Sha, S.; Minakuchi, K.; Higaki, N.; Sato, K.; Ohtsuki, K.; Kurata, A.; Yoshikawa, H.; J. Biochem. 121, 842-848, 1997

A;Title: Purification and characterization of glutaredoxin (thioltransferase) from rice

A;Reference number: JC5445; MUID:97335928; PMID:9192723

A;Accession: JC5445

A;Molecule type: mRNA

A;Residues: 1-112 <SHA1>

A;Cross-references: UNIPROT:P55142; UNIPARC:UPI000016DEAF

A;Accession: PC4325

A;Molecule type: protein

A;Residues: 2-5;8-106 <SHA2>

A;Cross-references: UNIPARC:UPI0000174DF0; UNIPARC:UPI0000174DF1

A;Experimental source: strain L. cv. Nipponbare

R;Minakuchi, K.; Yabushita, T.; Masumura, T.; Ichihara, K.; Tanaka, K. FEBS Lett. 337, 157-160, 1994

A;Title: Cloning and sequence analysis of a cDNA encoding rice glutaredoxin.

A;Reference number: S41736; MUID:94116670; PMID:8287970

A;Accession: S41736

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-33; 'G', 35-112 <MIN>

A;Cross-references: UNIPARC:UPI000012B7D4; GB:X77150; NID:9485952; PIDN:CAA54397.1; PID: C;Superfamily: Glutaredoxin; Glutaredoxin homology

C;Keywords: blocked amino end; electron transfer; redox-active disulfide

F;2-106/Product: glutaredoxin #status experimental <MAT>

F;5-96/Domain: glutaredoxin homology <GLUT>

F;2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #status

F;23-26/Disulfide bonds: redox-active #status predicted

Query Match 29.3%; Score 209; DB 2; Length 112;
Best Local Similarity 44.9%; Pred. No. 1.8e-11;
Matches 44; Conservative 17; Mismatches 33; Indels 4; Gaps 2;

Qy 41 VAHVKDLIGQKEVFAAKTCYPCATLSTLTFQELNVPKSKALVLELDMSGSEIQDAL 100
Db 3 LAKAKETVAGPVVVSYSKCPFC-VRVKLFPQLG---ATFKAIELDGSSELSQSL 58

Qy 101 EETSGQKTPNVYINGKHGNSDLETLKNGKLAEL 138
Db 59 AEWTGQRTVNVFNGKHIGGCDTTLALNKGKLVPLL 96

RESULT 6

S54825

C;Species: Ricinus communis (castor bean)

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S54825

R;Szederkenyi, J.; Schobert, C.
submitted to the EMBL Data Library, May 1995

A;Description: cDNA expressed in Ricinus cotyledons.

A;Reference number: S54825

A;Accession: S54825

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-102 <SZ>

A;Cross-references: UNIPROT:P55143; UNIPARC:UPI000012B7D9; EMBL:Z49699

C;Superfamily: Glutaredoxin; Glutaredoxin homology

C;Keywords: electron transfer; redox-active disulfide

F;5-96/Domain: glutaredoxin homology <GLUT>

F;23-26/Disulfide bonds: redox-active #status predicted

Query Match 28.4%; Score 203; DB 2; Length 102;
Best Local Similarity 46.8%; Pred. No. 5.4e-11;
Matches 44; Conservative 14; Mismatches 32; Indels 4; Gaps 2;

Qy 45 KDLIGQKEVFAAKTCYPCATLSTLTFQELNVPKSKALVLELDMSGSEIQDAL 104
Db 7 KELVSSNAVVFSTKYPCYC-TSVKLLDQLG---AKVKVELDTSDESIQTALAEWT 62

Qy 105 GQRTVPNVYINGKHGNSDLETLKNGKLAEL 138
Db 63 GQRTVPNVFNGKHIGGCDSTTAKHSQGLVPLL 96

RESULT 7

B84587

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: B84587

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: B84420; MUID:20083487; PMID:10617197

A;Accession: B84587

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-179 <STO>

A;Cross-references: UNIPROT:Q9SK75; UNIPARC:UPI00000A28C9; GB:AE002093; NID:94512708; PID: C;Genetics:

A;Gene: At2g20270

A;Map position: 2

Query Match 27.9%; Score 199; DB 2; Length 179;
Best Local Similarity 41.5%; Pred. No. 2.3e-10;
Matches 49; Conservative 24; Mismatches 39; Indels 6; Gaps 4;

Qy 23 RIATKRFSLTPKMVSQETVAH-VKDLIGQKEVFAAKTCYPCATLSTLTFQELNVPKSK 81
Db 56 RCSSVKAMSSSSSGSTLEETVKTVAENPVVYSKTCVSY-SSQVKSLSQLQV---E 111

Qy 82 ALVLELDMSGSEIQDAL 138
Db 112 PLVVELDQLGSEGSQLVLEKITQYTPNVFNGKHIGGCDSTLQLHNGKLEAIL 169

RESULT 8

G96802

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004

C;Accession: G96802

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96802

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-130 <STO>

A;Cross-references: UNIPROT:Q9FVX1; UNIPARC:UPI000009E782; GB:AE005173; NID:941079490; PID: C;Genetics:

A;Gene: F2P24.8

A;Map position: 1

C;Superfamily: glutaredoxin

Query Match 27.5%; Score 196; DB 2; Length 130;
Best Local Similarity 33.9%; Pred. No. 2.9e-10;
Matches 43; Conservative 30; Mismatches 46; Indels 8; Gaps 3;

Qy 12 IVIITITLPAITIAKRFSLTPKMVSQETVAHVKDLIGQKEVFAAKTCYPCATLSTL 71
Db 9 VVVAAILLP-----VVLCDLSNSAGANSVSFAFQNALNSKNKIVFSPKSYCYCLRS-KRI 63

Qy 72 FOELNVPKSKALVLELDMSGSEIQDAL 138
Db 63 GQRTVPNVFNGKHIGGCDSTTAKHSQGLVPLL 96

Search completed: November 6, 2006, 19:17:52
Job time : 42 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:08:49 ; Search time 301 Seconds
(without alignments)
439.459 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDSNLIVIIITLF.....DLFTLKNKGKLABILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	1	GLRX2 YEAST
2	391	54.8	110	1	GLRX1 YEAST
3	333	46.6	107	2	O6CUV6 KLULA
4	306.5	42.9	111	2	O751W5 ASHGO
5	300.5	42.1	119	2	Q5ABBI CANAL
6	276	38.7	104	2	Q6BIM4 DEBHA
7	271.5	38.0	105	2	Q6CCV8 YARLI
8	263	36.8	106	2	Q4IL11 GIBZE
9	253.5	35.5	156	2	Q3MPD5 CANAL
10	233.5	35.5	156	2	Q5AH29 CANAL
11	238.5	33.4	102	2	Q5B5G5 EMENI
12	232	32.5	113	2	Q6BT54 DEBHA
13	230.5	32.3	102	2	Q2UJ38 ASPOR
14	224	31.4	109	2	Q9P718 NEUCR
15	217	30.4	139	2	Q8S311 PROSI
16	216	30.3	136	2	Q6TU24 ORYSA
17	215	30.1	135	2	Q9M457 ARATH
18	212	29.7	101	1	GLRX1 SCHPO
19	212	29.7	102	2	Q4P415 USTMA
20	212	29.7	102	2	Q4JGJ1 ASPFU
21	211	29.6	596	2	Q66J56 XENLA
22	210	29.4	135	2	Q8LF06 ARATH
23	209	29.3	112	1	GLRX ORYSA
24	209	29.3	112	2	Q7FA28 ORYSA
25	208	29.1	113	2	Q94J59 DESAN
26	207	29.0	113	2	Q7XY25 WHEAT
27	207	29.0	600	2	Q7T2C8 BRACHYD
28	206	28.9	111	2	Q9FNE2 ARATH
29	203.5	28.5	125	2	Q8L8T2 ARABIDOP
30	203	28.4	102	1	GLRX RICCO
31	201	28.2	115	2	Q945T3 TILPL

RESULT 1

ID	GLRX2 YEAST	STANDARD;	PRT;	143 AA.
AC	P17695; Q6B234;			
DT	01-AUG-1990, integrated into UniProtKB/Swiss-Prot.			
DT	21-FEB-2006, sequence version 3.			
DT	07-MAR-2006, entry version 54.			
DE	Glutaredoxin-2, mitochondrial precursor (Thioltransferase)			
DE	(Glutathione-dependent oxidoreductase 2).			
GN	Name=GRX2; Synonyms=PTR, TTR1; OrderedLocusNames=YDR513W;			
GN	ORFNames=D9719.17;			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RC	STRAIN=DMY6;			
RX	MEDLINE=92412147; PubMed=1530649;			
RA	Gan Z.-R.;			
RT	"Cloning and sequencing of a gene encoding yeast thioltransferase.;"			
RL	Biochem. Biophys. Res. Commun. 187:949-955(1992).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=S288C;			
RX	MEDLINE=97313263; PubMed=9169867;			
RA	Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.,			
RA	Bargues M., Baron L., Becker A., Biteau N., Bloeker H., Blugeon C.,			
RA	Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F.,			
RA	Delaveau T., del Rey F., Dufon B., Eide L.G., Garcia-Cantalejo J.M.,			
RA	Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,			
RA	Hohelsel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C.,			
RA	Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,			
RA	Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,			
RA	Paulin L., Perez J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,			
RA	Prydz H., Purnelle B., Rasmussen S.W., Renacha M.A., Revuelta J.L.,			
RA	Rieger M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer M.,			
RA	Scharfe M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,			
RA	Soler-Mira A., Urrestazu L.A., Verhasselt P., Vissers S., Voet M.,			
RA	Volckaert G., Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S.,			
RA	Harris D.E., Bowman S., Brown D., Churcher C.M., Connor R., Dedman K.,			
RA	Gentles S., Hamlin N., Hunt S., Jones L., McDonald S., Murphy L.D.,			
RA	Niblett D., Odell C., Oliver K., Rajandream M.A., Richards C.,			
RA	Shore L., Walsh S.V., Barrell B.G., Dietrich F.S., Mulligan J.T.,			
RA	Allen E., Araujo R., Aviles E., Bero A., Carpenter J., Chen E.,			
RA	Cherry J.M., Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W.,			
RA	Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K.,			
RA	Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S.,			
RA	Schroeder M., Shogren T., Shroff N., Winant A., Yelton M.A.,			
RA	Botstein D., Davis R.W., Johnston M., Andrews S., Brinkman R.,			
RA	Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S.,			
RA	Greco T., Hallsworth K., Hawkins J., Hillier L.W., Jier M.,			
RA	Johnson D., Johnston L., Kirsten J., Kucaba T., Langston Y.,			
RA	Latrasille P., Le T., Mardis E., Menezes S., Miller N., Nhan M.,			

ALIGNMENTS

32	200	28.0	104	1	GLRX_VRRFO	081187 vernicia fo
33	199.5	27.9	146	2	Q55TF6 CRYNE	Q55tf6 cryptococcu
34	199	27.9	179	2	Q9SK75 ARATH	Q9sk75 arabidopsis
35	198.5	27.8	125	2	Q8RXH1 ARATH	Q8rxh1 arabidopsis
36	198	27.7	104	2	O50042 FRITAG	O50042 fritillaria
37	198	27.7	111	2	Q9FM49 ARATH	Q9fm49 arabidopsis
38	197.5	27.7	107	2	Q7YUB8 APHAV	Q7yub8 aphelecnhus
39	196.5	27.5	116	2	Q9W2D1 DROME	Q9w2d1 drosophila
40	196	27.5	130	2	Q6FVK1 ARATH	Q6fvk1 arabidopsis
41	195	27.3	134	2	Q6DH06 BRARE	Q6dh06 brachydanio
42	195	27.3	179	2	Q8LBS4 ARATH	Q8lbs4 arabidopsis
43	194	27.2	127	2	Q5AH28 CANAL	Q5ah28 candida alb
44	194	27.2	127	2	Q3MPD6 CANAL	Q3mpd6 candida alb
45	194	27.2	134	2	O65169 MESCR	O65169 mesembryant

RA Pauley A., Peluso D., Rifkin L., Riles L., Taich A., Trevasakis E.,
RA Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R.,
RA Waterson R., Albermann K., Hani J., Heumann K., Kleine K.,
RA Mewes H.-W., Zollner A., Zaccaria P.;
RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV.";
RL Nature 387:75-78(1997).
RN [3].
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP STRAIN=S288c;
RC MARSECHKY G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Marsetchky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA Labaer J.;
RT "Creation of the YFLEX clone resource: cloning of *Saccharomyces cerevisiae* ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [4].
RP PROTEIN SEQUENCE OF 36-141.
RX MEDLINE=90287489; PubMed=2189409;
RA Gan Z.-R., Polokoff M.A., Jacobs J.W., Sardana M.K.;
RT "Complete amino acid sequence of yeast thioltransferase (glutaredoxin).";
RL Biochem. Biophys. Res. Commun. 168:944-951(1990).
RN [5].
RP FUNCTION, AND INDUCTION.
RX PubMed=9571241;
RA Luikenhuis S., Perrone G., Dawes I.W., Grant C.M.;
RT "The yeast *Saccharomyces cerevisiae* contains two glutaredoxin genes that are required for protection against reactive oxygen species.";
RL Mol. Biol. Cell 9:1081-1091(1998).
RN [6].
RP INDUCTION.
RX PubMed=10786615;
RA Grant C.M., Luikenhuis S., Beckhouse A., Soderbergh M., Dawes I.W.;
RT "Differential regulation of glutaredoxin gene expression in response to stress conditions in the yeast *Saccharomyces cerevisiae*.";
RL Biochim. Biophys. Acta 1490:33-42(2000).
RN [7].
RP SUBCELLULAR LOCATION.
RX PubMed=11958675; DOI=10.1042/BJ20020570;
RA Pedrajas J.R., Porras P., Martinez-Gallisteo E., Padilla C.A.,
RA Miranda-Vizuet A., Barcena J.A.;
RT "Two isoforms of *Saccharomyces cerevisiae* glutaredoxin 2 are expressed in vivo and localize to different subcellular compartments.";
RL Biochem. J. 364:617-623(2002).
RN [8].
RP FUNCTION, AND BIOPHYSICO-CHEMICAL PROPERTIES.
RX PubMed=11875065; DOI=10.1074/jbc.M11686200;
RA Collinson E.J., Wheeler G.L., Garrido E.O., Avery S.V.,
RA Grant C.M.;
RT "The yeast glutaredoxins are active as glutathione peroxidases.";
RL J. Biol. Chem. 277:16712-16717(2002).
RN [9].
RP FUNCTION, AND BIOPHYSICO-CHEMICAL PROPERTIES.
RX PubMed=12684511; DOI=10.1074/jbc.M301387200;
RA Collinson E.J., Grant C.M.;
RT "Role of yeast glutaredoxins as glutathione S-transferases.";
RL J. Biol. Chem. 278:22492-22497(2003).
RN [10].
RP LEVEL OF PROTEIN EXPRESSION.
RX MEDLINE=22923965; PubMed=14562106; DOI=10.1038/nature02046;
RA Chaenaghams S., Hu W.-K., Bower K., Howson R.W., Belle A.,
RA Dephore N., O'Shea E.K., Weissman J.S.;
RT "Global analysis of protein expression in yeast.";
RL Nature 425:737-741(2003).
CC -!- FUNCTION: Multifunctional enzyme with glutathione-dependent oxidoreductase, glutathione peroxidase and glutathione S-transferase (GST) activity. The disulfide bond functions as an electron carrier in the glutathione-dependent synthesis of deoxyribonucleotides by the enzyme ribonucleotide reductase. In addition, it is also involved in reducing cytosolic protein- and nonprotein-disulfides in a coupled system with glutathione

CC reductase. Required for resistance to reactive oxygen species (ROS) by directly reducing hydroperoxides and for the detoxification of ROS-mediated damage.
CC -!- BIOPHYSICO-CHEMICAL PROPERTIES:
CC Kinetic parameters:
CC KM=2.0 mM for H(2)O(2);
CC KM=2.2 mM for tert-butyl hydroperoxide;
CC KM=0.87 mM for cumene hydroperoxide;
CC KM=0.17 mM for 1-chloro-2,4-dinitrobenzene;
CC KM=0.27 mM for 1,2-dichloro-4-nitrobenzene;
CC -!- SUBCELLULAR LOCATION: Cytoplasm, and mitochondrion. Two forms, a long and a short one are found in the mitochondrion, but only the short one is detected in the cytoplasm.
CC -!- INDUCTION: In response to exposure to reactive oxygen species (ROS) and upon entry into stationary phase.
CC -!- MISCELLANEOUS: Present with 31400 molecules/cell.
CC -!- MISCELLANEOUS: It is unclear whether the long polypeptide observed in mitochondria represents the immature form of the protein before cleavage of the transit peptide and release of the short form into the cytoplasm or whether two mature isoforms exists.
CC -!- SIMILARITY: Belongs to the glutaredoxin family.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: S45288; AAB23389.1; ALT_INIT; Genomic_DNA.
CC EMBL: U33057; AAB64953.1; -; Genomic_DNA.
CC EMBL: AY692896; AAT92915.1; -; Genomic_DNA.
CC PIR: S69570; GDBY.
CC HSSP: P44758; ILM3.
CC GeneOnline: L41005; -;
CC Ensembl: YDR513W; Saccharomyces cerevisiae.
CC SGD: S00002921; TTR1.
CC LinkHub: P17695; -;
CC GO: GO:0005829; C:cytosol; IDA.
CC GO: GO:0005739; C:mitochondrion; IDA.
CC GO: GO:0004602; F:glutathione peroxidase activity; IDA.
CC GO: GO:0004364; F:glutathione transferase activity; IDA.
CC GO: GO:0030508; F:thiol-disulfide exchange intermediate activity; IMP.
CC GO: GO:0030503; P:regulation of cell redox homeostasis; IDA.
CC GO: GO:0006979; P:response to oxidative stress; IMP.
CC PROSITE: PS00195; GLUTAREDOXIN; 1.
CC Complete proteome; Direct protein sequencing; Electron transport;
CC Mitochondrion; Redox-active center; Transit peptide; Transport.
CC TRANSIT 1 35 Mitochondrion.
CC CHAIN 36 143 Glutaredoxin-2.
CC FT DISULFID 61 64 Redox-active.
CC FT SEQUENCE 143 AA; 15861 MW; 99A79BB7695B2266 CRC64;
CC Query Match 100.0%; Score 714; DB 1; Length 143;
CC Best Local Similarity 100.0%; Pred. No. 3.1e-55;
CC Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 METNRSFDSNLVILIIITLFIATRIIAKFLSPKVMQSOETVAHVKDLIGQKEVFVAAKTY 60
CC DB 1 METNRSFDSNLVILIIITLFIATRIIAKFLSPKVMQSOETVAHVKDLIGQKEVFVAAKTY 60
CC QY 61 CPYCKATSLTLFQELNVPKSKALVLELDEMNSGSEIQDALEISGQKTVPNVYINGKHG 120
CC DB 61 CPYCKATSLTLFQELNVPKSKALVLELDEMNSGSEIQDALEISGQKTVPNVYINGKHG 120
CC QY 121 GNSDLETLLKNGKLAELIKPVFQ 143
CC DB 121 GNSDLETLLKNGKLAELIKPVFQ 143

CC RESULT 2
CC GLRX1 YEAST
CC ID GLRX1 YEAST STANDARD; PRT; 110 AA.
CC AC P25373;
CC DT 01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
CC DT 01-MAY-1992, sequence version 1.

RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.,
 RT "The diploid genome sequence of *Candida albicans*,"
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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CC -----
 CC EMBL: AACQ01000036; EAL00015.1; -; Genomic DNA.
 DR GO: 0005489; P:electron transporter activity; IEA.
 DR GO: 0005489; P:electron transporter activity; IEA.
 DR GO: 0005489; P:cell redox homeostasis; IEA.
 DR GO: 0006118; P:electron transport; IEA.
 DR InterPro: IPR011767; GLR AS.
 DR InterPro: IPR002109; Glutaredoxin.
 DR InterPro: IPR011899; GRX euk.
 DR InterPro: IPR012336; Thioridoxin-like fd.
 DR InterPro: IPR012335; Thioridoxin_fold.
 DR Pfam: PF00462; Glutaredoxin; 2.
 DR PRINTS: PR00160; GLUTAREDOXIN.
 DR TIGRFAMs: TIGR02180; GRX euk; 1.
 DR PROSITE: PS00195; GLUTAREDOXIN; UNKNOWN 1.
 DR KW Electron transport; Redox-active center; Transport.
 SQ SEQUENCE 119 AA; 13124 MW; 3B8431493A46565C CRC64;

Query Match 42.1%; Score 300.5; DB 2; Length 119;
 Best Local Similarity 50.4%; Pred. No. 1.2e-18;
 Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;

QY 19 LEATRIIAKPLSTPKMVSQETVAHVKDLIGQKEVFAAATYCPYCKATLSTLQELNVP 78

DB 1 MFT-LTKLFNTSTVSSQVKNVQELIKTPVFIASKSCYCPYCKATST-----IEAI 55

QY 79 KSKALVLELDEMSNGSBIQALBEISGQKTPVNVYINGKHIGNSDLETLKNGKLAEL 138

DB 56 TKDAYILELDEVDGAGIQLLEITQRTVPNVFIQGGHIGNSDVQALKSSDKLDDKI 115

QY 139 K 139

DB 116 K 116

RESULT 6

Q6BIM4_DBBHA

ID Q6BIM4_DBBHA PRELIMINARY; PRT; 104 AA.

AC Q6BIM4;

DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 17.

DE Similar to CA4919|Catrri Candida albicans Catrri1 Glutaredoxin.

GN OrderedLocNames=DEHAOG09966g;

OS Debaryomyces hansenii (Yeast) (Torulasporea hansenii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.

OX NCBI_TaxID=4959;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 36239 / CBS 767;

RX PubMed=15229592; DOI=10.1038/nature02579;

RA Lafontaine I., de Montigny J., March C., Neuvéglise C., Talla E.,

RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykascen C.,

RA Boissrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.,
 RT "Genome evolution in yeasts,"
 RL Nature 430:35-44(2004).

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CC -----
 CC EMBL: CR382139; CAG90415.1; -; Genomic DNA.
 DR GO: 0005489; P:electron transporter activity; IEA.
 DR GO: 0005489; P:cell redox homeostasis; IEA.
 DR GO: 0006118; P:electron transport; IEA.

DR InterPro: IPR011767; GLR AS.

DR InterPro: IPR002109; Glutaredoxin.

DR InterPro: IPR011899; GRX euk.

DR InterPro: IPR012336; Thioridoxin-like fd.

DR InterPro: IPR012335; Thioridoxin_fold.

DR Pfam: PF00462; Glutaredoxin; 2.

DR TIGRFAMs: TIGR02180; GRX euk; 1.

DR PROSITE: PS00195; GLUTAREDOXIN; UNKNOWN 1.

DR KW Complete proteome; Electron transport; Redox-active center; Transport.

SQ SEQUENCE 104 AA; 11393 MW; 1515F4DE0EAA896 CRC84;

Query Match 38.7%; Score 276; DB 2; Length 104;
 Best Local Similarity 52.3%; Pred. No. 1.6e-16;
 Matches 56; Conservative 20; Mismatches 27; Indels 4; Gaps 2;

QY 35 MVSQETVAHVKDLIGQKEVFAAATYCPYCKATLSTLQELNVPKSKALVLELDEMSNGS 94

DB 1 MVSQETTDKVKQLIKTPVFIASKSCYCPYCKATNTI---SSITKO-AYIILEDEVDGS 56

QY 95 EIQDALEESGQKTPVNVYINGKHIGNSDLETLKNGKLAELTKPV 141

DB 57 EIQEALYELTGQKTPVNVFIQGGHIGNSDVQELSGDKLESKIKAV 103

RESULT 7

Q6CCY8_YARLI

ID Q6CCY8_YARLI PRELIMINARY; PRT; 105 AA.

AC Q6CCY8;

DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 12.

DE Similar to sp|P17695|Saccharomyces cerevisiae Glutaredoxi.

GN OrderedLocNames=YALI0C05467g;

OS Yarrowia lipolytica (Candida lipolytica).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Dipodascaceae; Yarrowia.

OX NCBI_TaxID=4952;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=CLIB 122 / E 150;

RX PubMed=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., March C., Neuvéglise C., Talla E.,

RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykascen C.,

RA Boissrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

RA Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,

RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

RA Wincker P., Souciet J.-L.,

RT "Genome evolution in yeasts,"

RL Nature 430:35-44(2004).

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CC -----
DR EMBL; CR382129; CAG81775.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioredoxin-like fd.
DR InterPro; IPR006663; Thioredox dom2.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
DR Complete proteome.
KW Redox-active center; Transport.
SQ SEQUENCE 105 AA; 11427 MW; 95492161A6F90024 CRC64;

Query Match 38.0%; Score 271.5; DB 2; Length 105;
Best Local Similarity 48.6%; Pred. No. 4e-16;
Matches 51; Conservative 26; Mismatches 25; Indels 3; Gaps 1;

QY 35 MVSQETVAHVKDLIGKEVFAAKTCYPCYCKATLSTLFOELNVPKSKALVLELDMSNGS 94
Db 1 MATESAIKTIKEHAKDKVFAVSKSCYPCYCKTKQLLSQ---FKRAKPVILELDLDDGA 57

QY 95 EIQDALEIEISGQKTVPNVYINGKHGNSDLETLKXNGKLAELIK 139
Db 58 ELQAALAEITGQRTVNPVFIQGHGNSDLQVLAQKDELADKIK 102

RESULT 8
Q4IL11 GIBZE
ID Q4IL11 GIBZE PRELIMINARY; PRT; 106 AA.
AC Q4IL11.
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Hypothetical protein.
GN ORFNames=FG02097.1.
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084.
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnarre S., Graham M., Grand-Pierre N.,
RA Hafez N., Hagoopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kanat A.,
RA Karakas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lai A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
RA Maneus L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupback R., Seaman S., Severy P.,
RA Spirkov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Teafaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AACM01000111; EAA69728.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioredoxin-like fd.
DR InterPro; IPR006662; Thioredo.
DR InterPro; IPR006663; Thioredox dom2.
DR Pfam; PF00462; Glutaredoxin; 1.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
DR Complete proteome; Electron transport; Hypothetical protein;
KW Redox-active center; Transport.
SQ SEQUENCE 106 AA; 11646 MW; 162C3522D6205893 CRC64;

Query Match 36.8%; Score 263; DB 2; Length 106;
Best Local Similarity 56.2%; Pred. No. 2.3e-15;
Matches 54; Conservative 17; Mismatches 21; Indels 4; Gaps 2;

QY 44 VKDLIGQKEVFAAKTCYPCYCKATLSTLFOELNVPKSKALVLELDMSNGSITQDALEI 103
Db 8 VQQLDNNNSVVVFSKSCYPCYCKTKTL--DDLN---TEYELLEDEVAGSALQDALEKI 63

QY 104 SQGKTVPNVYINGKHGNSDLETLKXNGKLAELIK 139
Db 64 SGQRTVNPVYIKQGHGNSDLQSLNSGGLKNLLK 99

RESULT 9
Q3MPD5 CANAL
ID Q3MPD5 CANAL PRELIMINARY; PRT; 156 AA.
AC Q3MPD5.
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein Cad7.0240.
DE Name=Cad7.0240; ORFNames=CaO19.6509;
GN Candida albicans (Yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15937140; DOI=10.1534/genetics.104.034652;
RA Chibana H., Oka N., Nakayama H., Aoyama T., Magee B.B., Magee P.T.,
RA Mikami Y.;
RT "Sequence finishing and gene mapping for Candida albicans chromosome 7
RT and syntenic analysis against the Saccharomyces cerevisiae genome.";
RL Genetics 170:1525-1537(2005).
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CC -----
DR EMBL; AF006852; BAE44725.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX euk.
DR InterPro; IPR012336; Thioredoxin-like fd.
DR InterPro; IPR006662; Thioredo.
DR Pfam; PF00462; Glutaredoxin; 1.
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Query Match 35.5%; Score 253.5; DB 2; Length 156;
Best Local Similarity 40.3%; Pred. No. 2.4e-14;
Matches 56; Conservative 28; Mismatches 40; Indels 15; Gaps 5;

QY 4 NFSFSDNLVILIIITLPAITRIIAKFLSTPKMVSQETVAHVKDLIGQKEVFVAATKTCY 63
DB 32 SLISQPNFVMSLIGW-----LSSWFQNEP--ITPELKKETIESNINSHKVLVYSKSYCPY 84

QY 64 CKATLSTFLQELNVPKSKALVLEDEMSNGSIIQDALEESIQKQTPVNVYINGKHIGNS 123
DB 85 CTST-KTLQSLN---QDYKVIELDQIPKGSALQGLQELTGQRTVPNVFNGKHIGNS 140

QY 124 DLETLKNGKLAELIKPVF 142
DB 141 DIQALHSQK-----LKPLF 155

RESULT 11
Q5B5G5_EMENI PRELIMINARY; PRT; 102 AA.

ID Q5B5G5_EMENI AC Q5B5G5;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-MAR-2006, entry version 11.
DE Hypothetical protein.
GN ORFNames=AN4215.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=FGSC 4;
RX PubMed=16372000; DOI=10.1038/nature04341;
RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R., Batzoglou V., Lee S.-I., Basturkmen M., Spevak C.C., Clutterbuck J., Kapitonov S., Jurka J., Scacciochio C., Farman M., Butler J., Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C., Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S., Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U., Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T., Kungai T., Asai K., Machida M., Nierman W.C., Denning D.W., Caddick M., Hynes M., Paolletti M., Fischer R., Miller B.U., Dyer P.S., Sachs M.S., Osmari S.A., Birren B.W.;
RT "Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*.";
RL Nature 438.1105-1115(2005).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
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EMBL; AACQ01000069; EAA59314.1; -; Genomic DNA.
DR GO:0005489; F:electron transporter activity; IEA.
DR GO:0045454; P:cell redox homeostasis; IEA.
DR GO:0006118; P:electron transport; IEA.
DR InterPro: IPR002109; Glutaredoxin.
DR InterPro: IPR011899; GRX euk.
DR InterPro: IPR012336; Thioridoxin-like fd.
DR InterPro: IPR006662; Thioridoxin.
DR InterPro: IPR006663; Thioridoxin fold.
DR InterPro: IPR012335; Thioridoxin fold.
DR Pfam: PF00462; Glutaredoxin; 1.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
KW Hypothetical protein; Redox-active center.
SQ SEQUENCE 102 AA; 10960 MW; 91398F30245B16E3 CRC64;

Query Match 33.4%; Score 238.5; DB 2; Length 102;
Best Local Similarity 48.2%; Pred. No. 3.3e-13;

QY 4 NFSFSDNLVILIIITLPAITRIIAKFLSTPKMVSQETVAHVKDLIGQKEVFVAATKTCY 63
DB 32 SLISQPNFVMSLIGW-----LSSWFQNEP--ITPELKKETIESNINSHKVLVYSKSYCPY 84

QY 64 CKATLSTFLQELNVPKSKALVLEDEMSNGSIIQDALEESIQKQTPVNVYINGKHIGNS 123
DB 85 CTST-KTLQSLN---QDYKVIELDQIPKGSALQGLQELTGQRTVPNVFNGKHIGNS 140

QY 124 DLETLKNGKLAELIKPVF 142
DB 141 DIQALHSQK-----LKPLF 155

RESULT 10
Q5AH29_CANAL PRELIMINARY; PRT; 156 AA.

ID Q5AH29_CANAL AC Q5AH29;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Potential glutaredoxin.
GN Names=TR12; ORFNames=CaO19.13862, CaO19.6509;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
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EMBL; AACQ01000020; EAL02011.1; -; Genomic DNA.
DR EMBL; AACQ01000016; EAL02545.1; -; Genomic DNA.
DR GO:0005489; F:electron transporter activity; IEA.
DR GO:0045454; P:cell redox homeostasis; IEA.
DR GO:0006118; P:electron transport; IEA.
DR InterPro: IPR011767; GLR AS.
DR InterPro: IPR002109; Glutaredoxin.
DR InterPro: IPR011899; GRX euk.
DR InterPro: IPR012336; Thioridoxin-like fd.
DR InterPro: IPR006662; Thioridoxin.
DR InterPro: IPR012335; Thioridoxin fold.
DR Pfam: PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
KW Electron transport; Redox-active center; Transport.
SQ SEQUENCE 156 AA; 17779 MW; 6BA47C9B9702F6D8 CRC64;

Matches 53; Conservative 23; Mismatches 21; Indels 13; Gaps 4;

Qy 30 LSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 89
 Db 1 MSSAKVKAQQ-----IIDENGWVVFVSKSPYCKASKS--LLSELG--AKTYALELDT 49

Qy 90 MNSGSEIQDALEIEISGOKTVPNVYINGKHIGGNSDLETCLKNGKLAELIK 139
 Db 50 IDGADLQDALEIEISGOKTVPNVYIAKKHIGGNSDQGIKKO--LPALLK 97

RESULT 12

Q6BT54_DEBHA PRELIMINARY; PRT; 113 AA.

AC Q6BT54;
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Similar to ca|CA4964|IPF3920 Candida albicans IPF3920.
 GN OrderedLocNames=DEHA0D041365;
 OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 OX NCBI_TaxID=4959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36219 / CBS 767;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer E., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron R., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "genome evolution in yeasts";
 RL Nature 430:35-44 (2004).

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DR EMBL: CR382136; CAG86752.1; -; Genomic_DNA
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0045454; P:cell redox homeostasis; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPRO11767; GLR AS.
 DR InterPro: IPRO11895; GRX euk.
 DR InterPro: IPRO12336; Thioridoxin-like fd.
 DR InterPro: IPRO12335; Thioridoxin_dom2.
 DR Pfam: PF00462; Glutaredoxin; 2.
 DR PRINTS: PR00160; GLUTAREDOXIN.
 DR TIGRfam: TIGR02180; GRX_euk; 1.
 DR PROSITE: PS00195; GLUTAREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 113 AA; 12578 MW; 65A968395156E096 CRC64;

Query Match 32.5%; Score 232; DB 2; Length 113;
 Best Local Similarity 45.5%; Pred. No. 1.4e-12;
 Matches 50; Conservative 21; Mismatches 33; Indels 6; Gaps 3;

Qy 29 FLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 88
 Db 9 FVSPPP--VSPVKAQVQLNLSNKLIFLKSYPYCDST-KDLIKSIT---SDPKVVELN 62

Qy 89 EMSNGSEIQDALEIEISGOKTVPNVYINGKHIGGNSDLETCLKNGKLAELIK 138
 Db 63 TSANGRTIQDALEIEISGOKTVPNVYINFRKHIGGNSDQALQAGAKLSLV 112

RESULT 13

Q2UU38_ASPOR PRELIMINARY; PRT; 102 AA.

AC Q2UU38;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 3.
 DE Predicted protein.
 GN ORFNames=AQ0900090000473;
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NR16 40;
 RX PubMed=16372010; DOI=10.1038/nature04300;
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Goni K.,
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
 RA Galsagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhattacharya D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Maeda H., Maeyama N.,
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Komori T., Koyama Y., Minetoki T., Suhannan S., Tanaka A., Isono K.,
 RA Kuhara S., Ogasawara N., Kikuchi H.;
 RT "Genome sequencing and analysis of Aspergillus oryzae";
 RL Nature 438:1157-1161 (2005).

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DR EMBL: AP007150; BAE54927.1; -; Genomic_DNA
 KW Redox-active center.
 SQ SEQUENCE 102 AA; 10925 MW; 3FOA6BFB970952CD CRC64;

Query Match 32.3%; Score 230.5; DB 2; Length 102;
 Best Local Similarity 48.2%; Pred. No. 1.7e-12;
 Matches 53; Conservative 17; Mismatches 27; Indels 13; Gaps 3;

Qy 30 LSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 89
 Db 1 MSAAKIKAQ-----GIINANAVVFSKSPYCKSKSLLSQ-----LDKYLTIELDE 49

Qy 90 MNSGSEIQDALEIEISGOKTVPNVYINGKHIGGNSDLETCLKNGKLAELIK 139
 Db 50 ESDGSAIQDALEIEISGOKTVPNVYIFIKQKHIGGNSDLQARK--SELPALLK 97

RESULT 14

Q9P718_NEUCR PRELIMINARY; PRT; 109 AA.

AC Q9P718;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 07-MAR-2006, entry version 19.
 DE Probable glutaredoxin.
 GN Name=8D4.220;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 SQ SEQUENCE 109 AA; 12578 MW; 65A968395156E096 CRC64;

Query Match 32.5%; Score 232; DB 2; Length 113;
 Best Local Similarity 45.5%; Pred. No. 1.4e-12;
 Matches 50; Conservative 21; Mismatches 33; Indels 6; Gaps 3;

Qy 29 FLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFQELNVPKSKALVLELDE 88
 Db 9 FVSPPP--VSPVKAQVQLNLSNKLIFLKSYPYCDST-KDLIKSIT---SDPKVVELN 62


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RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL (2)
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; ALJ353819; CAB88564.1; -; Genomic_DNA.
DR PIR; T4748; T48748.
DR HSPP; P12309; LKTS.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX_euk.
DR InterPro; IPR012336; ThiOxdn-like_fd.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR TIGRFAMs; TIGR02180; GRX_euk; 1.
DR PROSITE; PS00194; GLUTAREDOXIN; 1.
DR PROSITE; PS00195; THIOREDOXIN; UNKNOWN_1.
DR Electron transport; Redox-active center; Transport.
KW SEQUENCE 109 AA; 11788 MW; 7E262272E84A1BE1 CRC64;

Query Match 31.4%; Score 224; DB 2; Length 109;
Best Local Similarity 42.6%; Pred. No. 6.8e-12;
Matches 46; Conservative 22; Mismatches 36; Indels 4; Gaps 1;

QY 36 VSQETVAHVLDIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLELDMSGSE 95
DB 1 MSDRAOTQAKQLINDNAVVFYSKSCPYCSNTK----QILDGLNAKYATVELNQESDGS 56

QY 96 IQDALEEISGQKTVPNVYINGKHIGNSDLETLLKNGKGLAEILKVPFQ 143
DB 57 VQDALLKLTGQRTVPNIFIGKHIGNSDLEAVVVGKNGKGGKIQELIQ 104

RESULT 15
Q8S3L1_9ROSI
ID Q8S3L1_9ROSI PRELIMINARY; PRT; 139 AA.
AC Q8S3L1;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 21-FEB-2006, entry version 19.
DE Glutaredoxin.
OS Populus tremula x Populus tremuloides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
OX NCBI_TaxID=47664;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21848454; PubMed=11858718; DOI=10.1006/prep.2001.1574;
RA Rouhier N., Gelhaye E., Sautiere P.E., Jacquot J.P.;
RT "Enhancement of poplar glutaredoxin expression by optimization of the
RT cDNA sequence.";
RL Protein Expr. Purif. 24:234-241(2002).
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CC -----
DR EMBL; AF483267; AAL90750.1; -; mRNA.
DR HSPP; P44758; 1NN3.
DR GO; GO:0005489; F:electron transporter activity; IEA.

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DR GO; GO:0045454; P:cell redox homeostasis; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR011767; GLR_AS.
DR InterPro; IPR002109; Glutaredoxin.
DR InterPro; IPR011899; GRX_euk.
DR InterPro; IPR012336; ThiOxdn-like_fd.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00462; Glutaredoxin; 2.
DR PRINTS; PR00160; GLUTAREDOXIN.
DR TIGRFAMs; TIGR02180; GRX_euk; 1.
DR PROSITE; PS00195; GLUTAREDOXIN; UNKNOWN_1.
DR Electron transport; Redox-active center; Transport.
KW SEQUENCE 139 AA; 15192 MW; C3527C3F1F94CB2D CRC64;

Query Match 30.4%; Score 217; DB 2; Length 139;
Best Local Similarity 35.5%; Pred. No. 3.7e-11;
Matches 49; Conservative 25; Mismatches 52; Indels 12; Gaps 3;

QY 1 METNFSFDSNLIVIIITLTPATRIIAKRFILSTPMVVSQETVAHVLDIGQKEVFVAAKTY 60
DB 1 MATRIRLPSILATAVTLTLAA-----SLTWAAGSPEATFVKKTISSHQIVIFSKEY 52

QY 61 CPYCKATLSTLFOELNVPKSKALVLELDMSGSEIQDALEEISGQKTVPNVYINGKHIG 120
DB 53 CPYCKKA-KGVFKELN---QTPHVVELDQREDGHDIDAMSEIVGRRTVPQVFDGKHIG 108

QY 121 GNSDLETLLKNGKGLAEIL 138
DB 109 GSDDTVEAYESGELAKLL 126

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Job time : 305 secs

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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:17:25 ; Search time 53 Seconds
(without alignments)
236.168 Million cell updates/sec

Title: US-10-523-362-4
Perfect score: 714
Sequence: 1 METNFSFSDNLVILIIITLF.....DLETLLKNGKLAEILKPVFQ 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC Celerra_SIDS3/prodata/2/iaa/5 COMB.pdp.*
2: /EMC Celerra_SIDS3/prodata/2/iaa/6 COMB.pdp.*
3: /EMC Celerra_SIDS3/prodata/2/iaa/7 COMB.pdp.*
4: /EMC Celerra_SIDS3/prodata/2/iaa/H COMB.pdp.*
5: /EMC Celerra_SIDS3/prodata/2/iaa/RTUS COMB.pdp.*
6: /EMC Celerra_SIDS3/prodata/2/iaa/RE COMB.pdp.*
7: /EMC Celerra_SIDS3/prodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.5	36.1	193	2	US-09-248-796A-18115
2	200	28.0	102	1	US-08-911-319A-4
3	200	28.0	102	2	US-09-352-619-4
4	196.5	27.5	137	2	US-09-270-767-32387
5	196.5	27.5	137	2	US-09-270-767-47604
6	174	24.4	60	2	US-09-248-796A-18114
7	173	24.2	114	2	US-09-621-976-5130
8	173	24.2	164	1	US-08-911-319A-1
9	173	24.2	164	2	US-09-352-619-1
10	151.5	21.2	106	2	US-09-162-564-3
11	146	20.4	94	2	US-09-621-976-5132
12	145	20.3	105	2	US-09-162-564-5
13	144.5	20.2	107	2	US-09-162-564-6
14	144	20.2	106	2	US-09-162-564-2
15	143	20.0	106	1	US-08-911-319A-3
16	143	20.0	106	2	US-09-352-619-3
17	143	20.0	106	2	US-09-162-564-4
18	143	20.0	106	2	US-09-513-999C-8053
19	142.5	20.0	105	2	US-09-538-092-1085
20	136	19.0	95	1	US-08-911-319A-5
21	135	19.0	95	2	US-09-352-619-5
22	129	18.1	115	2	US-09-902-540-10580
23	126.5	17.7	196	2	US-09-248-796A-18117
24	109.5	15.3	51	2	US-09-621-976-5131
25	108	15.1	95	2	US-09-328-352-8011
26	104.5	14.6	109	2	US-09-540-236-2497

27	103.5	14.5	86	2	US-09-252-991A-23535	Sequence 23535, A
28	103	14.4	93	2	US-09-489-039A-10745	Sequence 10745, A
29	103	14.4	291	2	US-09-270-767-33107	Sequence 33107, A
30	103	14.4	291	2	US-09-270-767-48324	Sequence 48324, A
31	98	13.7	106	2	US-09-902-540-10316	Sequence 10316, A
32	97.5	13.7	150	2	US-09-538-092-774	Sequence 774, App
33	90	12.6	270	2	US-09-540-236-2375	Sequence 2375, Ap
34	89.5	12.5	182	2	US-09-328-352-7369	Sequence 7369, Ap
35	89	12.5	147	2	US-09-294-539-14	Sequence 14, Appl
36	86.5	12.1	171	2	US-09-270-767-31780	Sequence 31780, A
37	86.5	12.1	171	2	US-09-270-767-46997	Sequence 46997, A
38	84	11.8	120	2	US-09-107-433-3440	Sequence 3440, Ap
39	83	11.6	93	2	US-09-248-796A-14244	Sequence 14244, A
40	83	11.6	115	2	US-09-583-110-3398	Sequence 3398, Ap
41	81	11.3	93	2	US-09-489-039A-10479	Sequence 10479, A
42	80.5	11.3	110	2	US-08-858-207A-273	Sequence 273, App
43	80	11.2	96	2	US-09-543-681A-5216	Sequence 5216, Ap
44	79	11.1	973	2	US-09-392-714-24	Sequence 24, Appl
45	79	11.1	976	2	US-09-104-324B-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-248-796A-18115
; Sequence 18115, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18115
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18115

Query Match 36.1%; Score 257.5; DB 2; Length 193;
Best Local Similarity 40.3%; Pred. No. 1.4e-22;
Matches 56; Conservative 29; Mismatches 39; Indels 15; Gaps 5;
Qy 4 NPSFSDNLVILIIITLFPATRIIAKRLSTPKMVSQETVAHVKDLIGQKEVFVAAKTCY 63
Db 69 SLSYQNFVMSLLIGW-----LSSWFQNEP--ITPELKEIESNINSHKVLVYSKVCY 121
Qy 64 CKATLSTLFLQELNVPKSKALVLEDEMSNGSEIQDALEEISGQKTVNPNVINGKHIGNS 123
Db 122 CTST-NTLLQSLN--QDVKVIEDQIPKGSALQNGQLQELTQRTVNPVINGKHIGNS 177
Qy 124 DLETLLKNGKLAEILKPVF 142
Db 178 DIQALHSQGK----LKPLF 192

RESULT 2
US-08-911-319A-4
; Sequence 4, Application US/08911319A
; Patent No. 5968798
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6


```
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 47604
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-47604

Query Match      27.5%; Score 196.5; DB 2; Length 137;
Best Local Similarity 37.6%; Pred. No. 1.8e-15;
Matches 44; Conservative 26; Mismatches 36; Indels 11; Gaps 4;

QY 30 LSTPKMVSQETVAH---VKDLIGOKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLE 86
DB 25 LQPTLVSDSSHAQFVRTISGNKVVFISKSYCPYC-SWAKEQFRKINV---KATVIE 80
QY 87 LDEMSNGSETQDALEISGQKTVPNVYINGKHGNSDLETLLKNGKLAELKPVFQ 143
DB 81 LDQRDDGNEIQAVLGEMTSRTPRCFIDGKFVGGGTDVKRLYEQG----ILQKYFQ 133

RESULT 6
US-09-248-796A-18114
; Sequence 18114, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18114
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18114

Query Match      24.4%; Score 174; DB 2; Length 60;
Best Local Similarity 57.9%; Pred. No. 2.6e-13;
Matches 33; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 84 VLEIDEMSGSETQDALEISGQKTVPNVYINGKHGNSDLETLLKNGKLAELKPK 140
DB 3 ILELDEVDGAEIQEALLEITGQRTVENVFIGGHGNSDVAQALNSIDLNKKFKP 59

RESULT 7
US-09-621-976-5130
; Sequence 5130, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
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; SEQ ID NO 5130
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5130

Query Match      24.2%; Score 173; DB 2; Length 114;
Best Local Similarity 36.7%; Pred. No. 8.8e-13;
Matches 36; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 41 VAHVKDLIGOKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLEIDEMSGSEIQDAL 100
DB 17 VNOIQETISDNCVIFSKTSCSYC-TWAKKLFHDMNV---NYKVELDLLEYGNQFQDAL 72
QY 101 EETSOGKTVPNVYINGKHGNSDLETLLKNGKLAEL 138
DB 73 YKMTGRTVPRIPVNGTFIGGATDTHRLHKEGKLLPLV 110

RESULT 8
US-08-911-319A-1
; Sequence 1, Application US/08911319A
; Patent No. 5968798
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,319A
; FILING DATE: August 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPLNOT03
; CLONE: 2447829
US-08-911-319A-1

Query Match      24.2%; Score 173; DB 1; Length 164;
Best Local Similarity 36.7%; Pred. No. 1.5e-12;
Matches 36; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 41 VAHVKDLIGOKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLEIDEMSGSEIQDAL 100
DB 57 VNOIQETISDNCVIFSKTSCSYC-TWAKKLFHDMNV---NYKVELDLLEYGNQFQDAL 112
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QY 101 EEISGQKTVPNVINGKHGNSDLETLKNGKLAETL 138
DB 113 YKMTGERTVPRIFVNGTFIGGATDTHRLHKEGKLLPLV 150

RESULT 9

US-09-352-619-1
; Sequence 1, Application US/09352619
; Patent No. 6084070
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,619
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829
US-09-352-619-1

Query Match 24.2%; Score 173; DB 2; Length 164;
Best Local Similarity 36.7%; Pred. No. 1.5e-12;
Matches 36; Conservative 22; Mismatches 36; Indels 4; Gaps 2;

QY 41 VAHVKDLIGQKEVFVAAKTCYCKATLSTLFQELNVPKSKALVLELDMSGSEIQDAL 100
DB 57 VNQIQETISDNCVWIFSKTSCSYC-TMAKKLFHDMNV---NYKVELDLLEYGNQFDAL 112

QY 101 EEISGQKTVPNVINGKHGNSDLETLKNGKLAETL 138
DB 113 YKMTGERTVPRIFVNGTFIGGATDTHRLHKEGKLLPLV 150

RESULT 10

US-09-162-564-3
; Sequence 3, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT

; TITLE OF INVENTION: OF OXIDATIVE DAMAGE IN OCULAR TISSUES
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-162-564-3

Query Match 21.2%; Score 151.5; DB 2; Length 106;
Best Local Similarity 35.3%; Pred. No. 3e-10; 37; Indels 5; Gaps 2;
Matches 36; Conservative 24; Mismatches 24; Indels 5; Gaps 2;
QY 42 AHVKDLIGQKEVFVAAKTCYCKATLSTLFQELNVPKSKALV--LELDMSGSEIQDA 99
DB 4 AFVNSKIOPGVVFIKPTCFCKTKOELLQ--LPPKEGLLEFVDITATSDTNEIQDY 60
QY 100 LEEISGQKTVPNVINGKHGNSDLETLKNGKLAETL 141
DB 61 LQOLTGARTVPRVFICGICIGCTDLESMMKRGELLTLQOI 102

RESULT 11

US-09-621-976-5132
; Sequence 5132, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5132
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5132

Query Match 20.4%; Score 146; DB 2; Length 94;
Best Local Similarity 37.0%; Pred. No. 1.1e-09;
Matches 30; Conservative 19; Mismatches 28; Indels 4; Gaps 2;

QY 41 VAHVKDLIGQKEVFVAAKTCYCKATLSTLFQELNVPKSKALVLELDMSGSEIQDAL 100
DB 17 VNQIQETISDNCVWIFSKTSCSYC-TMAKKLFHDMNV---NYKVELDLLEYGNQFDAL 72

QY 101 EEISGQKTVPNVINGKHGIGG 121
DB 73 YKMTGERTVPRIFVNGTFIGG 93

RESULT 12

US-09-162-564-5
; Sequence 5, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-162-564-5

Query Match      20.2%; Score 145; DB 2; Length 105;
Best Local Similarity 37.4%; Pred. No. 1.8e-09;
Matches 37; Conservative 18; Mismatches 40; Indels 4; Gaps 2;

QY 42 AHVKDLIGQKEVFAAATYCPYCKATLSTLFOELNVPKSKAL-VLELDEMSGSEIODAL 100
Db 4 AFVNSKIQPGKVVVFIKPTCPYCKRQELLSQ---LPFKQLLEFVDITATSDN 60

QY 101 EISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIK 139
Db 61 QQLTGARTVPRVFIGQECIGGCTDLVNMHGERGELLTRLK 99

RESULT 13
US-09-162-564-6
; Sequence 6, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-162-564-6

Query Match      20.2%; Score 144.5; DB 2; Length 107;
Best Local Similarity 36.7%; Pred. No. 2.1e-09;
Matches 36; Conservative 20; Mismatches 37; Indels 5; Gaps 2;

QY 44 VKDLIGQKEVFAAATYCPYCKATLSTLFOELNVPKSKALV--LELDEMSGSEIODALE 101
Db 6 VNSKIQPGKVVVFIKPTCPYCKRQELLSQ---LPFKQLLEFVDITATSDN 62

QY 102 EISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIK 139
Db 63 QLTGARTVPRVFLGKDCIGGSDLIAMQEKGLLARLK 100

RESULT 14
US-09-162-564-2
; Sequence 2, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-162-564-2

; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-162-564-5

Query Match      20.2%; Score 144; DB 2; Length 106;
Best Local Similarity 35.2%; Pred. No. 2.4e-09;
Matches 38; Conservative 27; Mismatches 35; Indels 8; Gaps 4;

QY 36 VSOETVAHVKDLIGQKEVFAAATYCPYCKATLSTLFOELNVPKSKALV--LELDEMSG 93
Db 1 MAQEFV-NCKIQPGKVVFI--KPTCPFCVKTQELLSQ---LPFKQLLEFVDITATSDT 54

QY 94 SEIQDALEISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIKPV 141
Db 55 NEIQDYLOQLTGARTVPRVFIGKEICGGCTDLESMMHKGELLTRLQOI 102

RESULT 15
US-08-911-319A-3
; Sequence 3, Application US/08911319A
; Patent No. 5968798
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,319A
; FILING DATE: August 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-4166
; TELEFAX: 650-855-0555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 531405
US-08-911-319A-3

Query Match      20.0%; Score 143; DB 1; Length 106;
Best Local Similarity 35.2%; Pred. No. 3.1e-09;
Matches 38; Conservative 27; Mismatches 35; Indels 8; Gaps 4;

QY 36 VSOETVAHVKDLIGQKEVFAAATYCPYCKATLSTLFOELNVPKSKALV--LELDEMSG 93
Db 1 MAQEFV-NCKIQPGKVVFI--KPTCPYCRRAQELLSQ---LPKQGLLEFVDITATNHT 54

QY 94 SEIQDALEISGQKTPNVYINGKHIGGNSDLETLKNGKLAELIKPV 141
Db 55 NEIQDYLOQLTGARTVPRVFIGKDCIGGSDLVLSQQSGELLTRLQOI 102
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Search completed: November 6, 2006, 19:18:51
Job time : 54 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:23:26 ; Search time 451 Seconds
(without alignments)
6678.517 Million cell updates/sec

Title: US-10-523-362-3

Perfect score: 432

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Post-processing: Minimum Match 0%

Maximum Match 100%

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15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	100.0	432	12	Adk90658 Baker's Y
2	432	100.0	432	13	Adt87074 Yeast Str
3	432	100.0	932	6	Abq76354 S. cerevi
4	147.4	34.1	833	6	Abq76320 S. cerevi
5	143.4	33.2	333	12	Adk90656 Baker's Y
6	89	20.6	360	6	Abq76591 C. albica
7	89	20.6	360	6	Abz32493 Candida a
8	64.6	15.0	621	2	Adr02454 A. gossyp
9	57.8	13.4	440	8	Abz53183 Aspergill
10	56	13.0	531	11	Adk32590 Rice abio
11	55.6	12.9	733	13	Adk90702 Rice oxid
12	55.2	12.8	619	3	Aac43844 Arabidops
13	55	12.7	278	7	AdS70498 Corn seed
14	55	12.7	392	14	Aeb55134 Rice geno
15	55	12.7	628	12	Adk90700 Rice oxid
16	54.8	12.7	309	13	Adr85786 Aspergill
17	54.8	12.7	336	12	Adk90680 Thale cre
18	54.8	12.7	378	3	Aac48716 Arabidops

19	54.8	12.7	608	3	AAC32667	Arabidops
20	54.8	12.7	636	3	AAC48717	Arabidops
21	54.4	12.6	594	3	AAC44274	Arabidops
22	53.2	12.3	628	3	AAC40081	Arabidops
23	53.2	12.3	657	12	ADK90670	Rape oxid
24	51.2	11.9	7337	13	ADR84319	Aspergill
25	50	11.6	540	12	ADK90688	Thale cre
26	50	11.6	707	3	AAC47504	Arabidops
27	50	11.6	709	3	AAC34109	Arabidops
28	49.2	11.4	512	6	ABK71699	Human dit
29	49.2	11.4	621	13	ADK33976	Plant ful
30	49.2	11.4	864	13	ADK50598	Plant ful
31	46.8	10.8	385	12	ADP92474	Cotton ex
32	46.8	10.8	590	13	ACN53628	Cotton an
33	46.4	10.7	529	12	ADP91617	Cotton ex
34	45.6	10.6	446	4	ABL13599	Drosophil
35	45.6	10.6	478	4	ABL11847	Drosophil
36	45.6	10.6	2446	4	ABL13598	Drosophil
37	45.4	10.5	672	12	ADK90674	Rape oxid
C 38	45	10.4	550	13	ACN61980	Cotton gy
C 39	44.8	10.4	479	5	AAH87770	Peppermin
C 40	44.6	10.3	832	13	ADT19470	Plant CDN
41	44	10.2	302	10	ABX85625	Corn ear-
C 42	44	10.2	535	11	ACL30824	Rice abio
C 43	43.8	10.1	343	13	ACN49246	Cotton pr
44	43.8	10.1	501	5	AAH87771	Peppermin
45	43.8	10.1	546	13	ACN47600	Cotton pr

ALIGNMENTS

RESULT 1

ADK90658

ID ADK90658 standard; cDNA; 432 BP.

XX AC ADK90658;

DT 20-MAY-2004 (first entry)

XX DE Baker's yeast glutaredoxin 2 (GRX2) cDNA SeqID 3.

XX KW baker's yeast; GRX2; gene; ss; transgenic; abiotic stress response;
KW crop plant; oxidoreductase stress-related protein; ORSRP;
KW environmental stress; salinity; drought; temperature; chemical; pathogen;
KW glutaredoxin; GRX; thioredoxin; THX; Quantitative Trait Locus; QTL.
XX OS Saccharomyces cerevisiae.
XX PN WO2004018687-A2.
XX PD 04-MAR-2004.
XX PF 01-JUL-2003; 2003WO-EP006994.
XX PR 07-AUG-2002; 2002BP-00017671.
XX PA (BADI) BASF PLANT SCI GMBH.
XX PI Chardonnais A, Puzio P;
XX DR WPI; 2004-226856/21.
XX DR P-PSDB; ADK90659.
XX PT New transgenic plant cell transformed by oxidoreductase stress-related
XX protein (ORSRP) coding nucleic acid, useful for producing a transgenic
XX plant with increased environmental stress tolerance.
XX PS Claim 5; SEQ ID NO 3; 140pp; English.
XX CC This invention relates to novel transgenic plant cells transformed by
XX genes encoding proteins associated with the abiotic stress response.
XX CC Specifically, it refers to transgenic crop plants expressing the

```
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thioredoxin (TRX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polynucleotide
CC sequence is a baker's yeast GRX cDNA of the invention.
XX
SQ Sequence 432 BP; 142 A; 81 C; 85 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 432; DB 12; Length 432;
Best Local Similarity 100.0%; Pred. NO. 4e-112;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAATGTTATTATCATTCACGTTGTTT 60
Db 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAATGTTATTATCATTCACGTTGTTT 60

Qy 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120
Db 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120

Qy 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180

Qy 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGGAACGTTCCCAATCC 240
Db 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGGAACGTTCCCAATCC 240

Qy 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGTTTA 300
Db 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGTTTA 300

Qy 301 GAAGAAATCTCGGCCCAAAAACCTGTACCTAACGTTATACATCAATGCGCAAGCATGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACCTGTACCTAACGTTATACATCAATGCGCAAGCATGGT 360

Qy 361 GGTAAACGCAATTTGGAACTTTGAGAAAAATGGCAAAATGGCAAGTTAGTGAATTTGAAGCCG 420
Db 361 GGTAAACGCAATTTGGAACTTTGAGAAAAATGGCAAAATGGCAAGTTAGTGAATTTGAAGCCG 420

Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432

RESULT 2
ADT87074
ID ADT87074 standard; DNA; 432 BP.
XX
AC ADT87074;
XX
13-JAN-2005 (first entry)
XX
Yeast Stress-related protein gene YEL045C.
XX
Yeast; Stress-related protein; SRP; ds; gene; environmental stress;
XX abiotic stress; drought; heat; cold; salt.
XX Saccharomyces cerevisiae.
XX
PN W02004092398-A2.
XX
PD 28-OCT-2004.
XX
PF 15-APR-2004; 2004WO-US011888.
XX
PR 15-APR-2003; 2003EP-00008080.

107 MAY-2003; 2003BP-00039728.
108 AUG-2003; 2003EP-00016672.
109 SEP-2003; 2003EP-00022225.
(BADI ) BASF PLANT SCI GMBH.
Puzio P, Chardonens A, Shirley A, Wang X, Sarria-Millan R;
Mckersie B, Chen R;
WPI; 2004-766883/75.
P-P8DB; ADT87075.
New isolated nucleic acid molecule comprises a sequence encoding Stress-
Related Protein (SRP), useful for producing transformed plants with
altered metabolic activity resulting in increased tolerance or resistance
to environmental stress.
Claim 20; SEQ ID NO 52; 911pp; English.
The invention relates an isolated nucleic acid molecule comprises a
nucleic acid molecule encoding a Stress-Related Protein (SRP), from Yeast
or E. coli and their homologues from Rice, Soybean and Rape. Also
included are a transformed plant cell with altered metabolic activity
compared to a corresponding non-transformed wild type plant cell (where
the metabolic activity is altered by transformation with a SRP coding
nucleic acid and results in increased tolerance and/or resistance to an
environmental stress as compared to a corresponding non-transformed wild
type plant cell), a transgenic plant generated from the plant cell above
(and which is a monocot or dicot plant, or a gymnosperm plant), a seed
produced by a transgenic plant above (where the seed is genetically
homologous for a transgene conferring altered metabolic activity
resulting in an increased tolerance to environmental stress as compared
to a corresponding non-transformed wild type plant), a nucleic acid
construct which confers the expression of the nucleic acid molecule above
(comprising one or more regulatory elements, where expression of the SRP
coding nucleic acid in a host cell results in altered metabolic activity
resulting in increased tolerance to environmental stress as compared to a
corresponding non-transformed wild type host cell), a vector comprising
the nucleic acid molecule above or the nucleic acid construct, a host
cell which has been transformed stably or transiently with the vector (or
the nucleic acid molecules above, or the nucleic acid construct), an
isolated Stress Related Protein (SRP) selected from the amino acid
sequences fully given in the specification and/or its homologues, a
method of producing a transgenic plant with altered metabolic activity
compared to a corresponding non-transformed wild type plant cell,
modifying stress tolerance of a plant, detecting environmental stress in
plant cells or plants, screening plant cells or plants for increased
tolerance and/or resistance to environmental stress, breeding plant cells
or plants towards increased tolerance and/or resistance to environmental
stress, increasing tolerance of a plant to at least one abiotic stress,
a plant transformed with the nucleic acids above and a seed of the plant.
The altered metabolic activity and/or a SRP encoding nucleic acids or its
homologues are useful as markers for selection of plants or plant cells
with increased tolerance to environmental stress, or for detection of
stresses in plants or plant cells. The nucleic acids are useful for
producing transformed plants with altered metabolic activity resulting in
increased tolerance and/or resistance to an environmental stress
(drought, heat, cold and salt) as compared to a corresponding non-
transformed wild-type plant cell. The present sequence is a yeast gene
encoding an SRP of the invention.
Sequence 432 BP; 142 A; 81 C; 85 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 432; DB 13; Length 432;
Best Local Similarity 100.0%; Pred. NO. 4e-112;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAATGTTATTATCATTCACGTTGTTT 60
Db 1 ATGGAGACCAATTTTCCTTCGACTCGAATTTAATGTTATTATCATTCACGTTGTTT 60

Qy 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120
Db 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGAAACA 120

Qy 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAGAAAGTGTGTTGTCAGCAAGACATAC 180

Qy 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGGAACGTTCCCAATCC 240
Db 181 TSCCCTTACTGAAGCTACTTGTCTACCCCTCTCCAGAAATGGAACGTTCCCAATCC 240

Qy 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGTTTA 300
Db 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGTTTA 300

Qy 301 GAAGAAATCTCGGCCCAAAAACCTGTACCTAACGTTATACATCAATGCGCAAGCATGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACCTGTACCTAACGTTATACATCAATGCGCAAGCATGGT 360

Qy 361 GGTAAACGCAATTTGGAACTTTGAGAAAAATGGCAAAATGGCAAGTTAGTGAATTTGAAGCCG 420
Db 361 GGTAAACGCAATTTGGAACTTTGAGAAAAATGGCAAAATGGCAAGTTAGTGAATTTGAAGCCG 420

Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432

RESULT 2
ADT87074
ID ADT87074 standard; DNA; 432 BP.
XX
AC ADT87074;
XX
13-JAN-2005 (first entry)
XX
Yeast Stress-related protein gene YEL045C.
XX
Yeast; Stress-related protein; SRP; ds; gene; environmental stress;
XX abiotic stress; drought; heat; cold; salt.
XX Saccharomyces cerevisiae.
XX
PN W02004092398-A2.
XX
PD 28-OCT-2004.
XX
PF 15-APR-2004; 2004WO-US011888.
XX
PR 15-APR-2003; 2003EP-00008080.
```

Db 61 GCCAAGAAGATTATGCTAAAGATTTTATCTACTCTCAAAAATGGTATCCCGAAGAAC 120
Qy 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Qy 181 TGGCTTACTGTAAGCTACTTTGTCCTACCCCTTCCAGAAATGAACGTTCCCAATCC 240
Db 181 TGGCTTACTGTAAGCTACTTTGTCCTACCCCTTCCAGAAATGAACGTTCCCAATCC 240
Qy 241 AAGSCCTCTGTTGGAAATAGATGAATGAGCAATGGCTCAGATTCAGACGCTTTA 300
Db 241 AAGSCCTCTGTTGGAAATAGATGAATGAGCAATGGCTCAGATTCAGACGCTTTA 300
Qy 301 GAAGAAATCTCGGCGCCAAAACCTGTACCTTAAGCTATACATCAATGCGCAAGCATTTGGT 360
Db 301 GAAGAAATCTCGGCGCCAAAACCTGTACCTTAAGCTATACATCAATGCGCAAGCATTTGGT 360
Qy 361 GGTACAGCGATTGGAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 420
Db 361 GGTACAGCGATTGGAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 420
Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432

RESULT 3
ABQ76354
ID ABQ76354 standard; cDNA; 932 BP.
XX AC ABQ76354;
XX DT 21-NOV-2002 (first entry)
XX DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 133.
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX Saccharomyces cerevisiae.
XX WO200264766-A2.

22-AUG-2002.
XX 21-DEC-2001; 2001WO-EP015398.
XX 22-DEC-2000; 2000EP-00870318.
PR 04-JAN-2001; 2001EP-00870002.
PR 09-JAN-2001; 2001EP-00870003.
XX (JANC) JANSSEN PHARM NV.
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX WPI; 2002-667002/71.
DR P-PSDB; ABG93088.
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX Claim 36; Fig 1; 344pp; English.
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or

CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention
XX
SQ Sequence 932 BP; 270 A; 220 C; 158 G; 284 T; 0 U; 0 Other;
Query Match 100.0%; Score 432; DB 6; Length 932;
Best Local Similarity 100.0%; Pred. No. 5.1e-112;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGACCAATTTTCTTCGACTCGAATTTAAATGTTTATTATCATCATCAGTTGTTT 60
Db 501 ATGGAGACCAATTTTCTTCGACTCGAATTTAAATGTTTATTATCATCATCAGTTGTTT 560
Qy 61 GCCACAAGAAATATTGCTAAAAAGATTTTATCTACTCCAAAATGGTATCCCGAAGAAC 120
Db 561 GCCACAAGAAATATTGCTAAAAAGATTTTATCTACTCCAAAATGGTATCCCGAAGAAC 620
Qy 121 GTTGCTCAGTAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 621 GTTGCTCAGTAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 680
Qy 181 TGGCTTACTGTAAGCTACTTTGTCCTACCCCTTCCAGAAATGAACGTTCCCAATCC 240
Db 681 TGGCTTACTGTAAGCTACTTTGTCCTACCCCTTCCAGAAATGAACGTTCCCAATCC 740
Qy 241 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 741 AAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 800
Qy 301 GAAGAAATCTCGGCGCCAAAACCTGTACCTTAAGCTATACATCAATGCGCAAGCATTTGGT 360
Db 801 GAAGAAATCTCGGCGCCAAAACCTGTACCTTAAGCTATACATCAATGCGCAAGCATTTGGT 860
Qy 361 GGTACAGCGATTGGAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 420
Db 861 GGTACAGCGATTGGAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTTGAAGCCG 920
Qy 421 GTATTTCAATAG 432
Db 921 GTATTTCAATAG 932

RESULT 4
ABQ76320
ID ABQ76320 standard; cDNA; 833 BP.
XX AC ABQ76320;
XX DT 21-NOV-2002 (first entry)
XX DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 65.
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX Saccharomyces cerevisiae.
XX WO200264766-A2.

XX 22-AUG-2002.
PD
XX 21-DEC-2001; 2001WO-EP015398.
PF
XX 22-DEC-2000; 2000EP-00870318.
PR
XX 04-JAN-2001; 2001EP-00870002.
PR
XX 09-JAN-2001; 2001EP-00870003.
PR
XX (JANC) JANSSEN PHARM NV.
PA
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX WPI; 2002-667002/71.
DR
XX P-PSDB; ABG93054.
DR
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX
XX Claim 36; Fig 1; 344pp; English.
PS
XX This invention describes a novel nucleic acid representing a synthetic
XX Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying Bax-
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC leukaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention
XX
XX Sequence 833 BP; 278 A; 171 C; 152 G; 232 T; 0 U; 0 Other;
SQ
Query Match 34.1%; Score 147.4; DB 6; Length 833;
Best Local Similarity 65.2%; Pred. No. 2.1e-31;
Matches 217; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 99 AAAAAATGGTATCCAGGAAACAGTTCCTCACGTAAGGATCTGATGGCCAAAGGAAGT 158
DB 497 AAAAAATGGTATCTCAAGAACTATCAAGCAGCGTCAAGGACCTATTATGCGAAGAACGAGAT 556
QY 159 GTTTGTTGAGCAAGACATCTAGCCCTTACTGTAAGCTACTTTGCTACCTCTTCCA 218
DB 557 CTTGCGTCGATCCAAACGCTACTGTCTCATCTGCGCATGCGCCCTTAACACGCTTTTGA 616
QY 219 AGAATTGAAGCTTCCCAATCCAAAGCCCTTGTTGGAAATTAGATGAATGAGCAATGG 278
DB 617 AAGTTTAAGGTTCCAGGTCCTCAAGGTTCTGGTTTTCGATTTGAATGACATGAGGAAGG 676
QY 279 CTCAGAGATTCAAGACGCTTTTGAAGAAATCTCGGGCCAAAGAAATCTGTACCTTAACGTATA 338
DB 677 CGCAGACATTCAGGCTCGCTTATATGAGATTAAATGCGCCAAAGAACCGTGCCAAACATCTA 736
QY 339 CATCAATGCGACGACATTTGGTGGTAAACAGCGATTTGGAACTTTGAAAGAAATGCGCAA 398
DB 737 TATTAATGTTAAACATATTGGAGGCAACGACGATTTGCGAGGAATTGAGGGAGACTGGTGA 796
QY 399 GTTAGCTGAAATATTGAAGCCGGTATTTCAATA 431
DB 797 ATTGGAGGAATTGTTAGAACCTATTCTTCGAAA 829

RESULT 5
ADK90656
ID ADK90656 standard; cDNA; 333 BP.
XX
XX ADK90656;
AC
XX 20-MAY-2004 (first entry)
DT
XX Baker's yeast glutaredoxin 1 (GRX1) cDNA seqid 1.
DE
XX baker's yeast; GRX1; gene; ss; transgenic; abiotic stress response;
KW crop plant; oxidoreductase stress-related protein; ORSRP;
KW environmental stress; salinity; drought; temperature; chemical; pathogen;
KW glutaredoxin; GRX; thioredoxin; THX; Quantitative Trait Locus; QTL.
OS Saccharomyces cerevisiae.
XX
XX WO2004018687-A2.
PN
XX 04-MAR-2004.
PD
XX 01-JUL-2003; 2003WO-EP006994.
PF
XX 07-AUG-2002; 2002EP-00017671.
PR
XX (BADI) BASF PLANT SCI GMBH.
PA
XX Chardonnens A, Puzio P;
PI
XX WPI; 2004-226856/21.
DR
XX P-PSDB; ADK90657.
DR
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
XX
XX Claim 5; SEQ ID NO 1; 140pp; English.
PS
XX This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polynucleotide
CC sequence is a baker's yeast GRX cDNA of the invention.
XX
XX Sequence 333 BP; 110 A; 64 C; 75 G; 84 T; 0 U; 0 Other;
SQ

Query Match 33.2%; Score 143.4; DB 12; Length 333;
Best Local Similarity 64.7%; Pred. No. 2.1e-30;
Matches 213; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 103 ATGGTATCCAGGAAACAGTTCCTCACGTAAGGATCTGATGGCCAAAGGAAGTGT 162
DB 1 ATGGTATCTCAAGAACTATCAAGCAGCGTCAAGGACCTATTATGCGAAGAACGAGATCTTC 60
QY 163 GTTGACAGAAAGACATCTAGCCCTTACTGTAAGCTACTTTGCTACCTCTTCCAAGAA 222
DB 61 GTCGATCTCAAAACGATCTGTCCATCTGCGCATGCGCCCTAAACACGCTTTTGAAG 120
QY 223 TTGAACGTTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCA 282
DB 121 TTAAAGGTTCCAGGTCCAAAGTTCGTGTTTGTCAATGAATGACATGAAGGAGGCGCA 180

QY 283 GAGATTCAAGACGCTTTAGAGAAATCTCGGGCAAAAACCTGTACTTAACGTATACATC 342
Db 181 GACATTGAGCTGGTGTATATGAGATTAAATGGCCAAAGAACCGTGGCCAAACATCTATATT 240
QY 343 AATGGCAAGCACATTGGTGTAAACAGCGATTTCGAACTTTGAGAAATGCGCAAGTTA 402
Db 241 AATGGTAAACATATTGGAGCAACGACGACTTGAGGAATTGAGGAGACTGGTGAATTG 300
QY 403 GCTCAATATTGAAGCGGTATTTCATA 431
Db 301 GAGGAATTGTTAGAACCTATTCTTGCAA 329

RESULT 6
ABQ76591
ID ABQ76591 standard; cDNA; 360 BP.
XX AC ABQ76591;
XX DT 21-NOV-2002 (first entry)
XX C. albicans BAX-associated cDNA fragment SEQ ID 607.
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotrophic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX Candida albicans.
XX WO200264766-A2.
XX 22-AUG-2002.
XX 21-DEC-2001; 2001WO-EP015398.
XX 22-DEC-2000; 2000EP-00870318.
PR 04-JAN-2001; 2001EP-00870002.
PR 09-JAN-2001; 2001EP-00870003.
XX (JANC) JANSSEN PHARM NV.
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX WPI; 2002-667002/71.
DR P-PSDB; ABG93325.
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX Claim 36; Fig 2; 344pp; English.
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi; identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotrophic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene

CC described in the disclosure of the invention
XX Sequence 360 BP; 129 A; 68 C; 62 G; 101 T; 0 U; 0 Other;
SQ

Query Match 20.6%; Score 89; DB 6; Length 360;
Best Local Similarity 55.4%; Pred. No. 5.6e-15;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;
QY 67 AGAATATTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCAGGAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGAGACTATTCAATACATCAACAATGTTTCTCTCAAGTTAAGAAC 69
QY 127 CAGTAAAGATCTGATGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATACCTCCCT 186
Db 70 AAGTCAACAATTTGATCAAAACCAACCAAGTTTCAATGGCTCCAAATCTTATTGTCCA 129
QY 187 TACTGTAAAGCTACTTTTGTCTACCTCTTCCAAAGATTGAAAGTTCCCAATCCAAGGCC 246
Db 130 TACTGTAAAGCTACTTAAAGCTCTTCCAAAGCTCTTCCAAAGCTTAAAGAGGATGCT 177
QY 247 CTGTGTTGGAATTTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAA 306
Db 178 TACATTTCTGAAATTAGACGAGTTGAGGAGCGTGTGAATCCAAAGAGCATTTATTGGAA 237
QY 307 ATCTCGGCAAAAACCTGTACTTAACGTATACATCAATGCGCAAGCACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAAATGCTTTTATTGGTGGTCAACATATTGGTGGCAAT 297
QY 367 AGCGATTTGGAACCTTTGAAGAAATGCAAGTTAGCTGAATATTGAAGCGGTTATTT 426
Db 298 TCGATGTGCAAGCTTTGAAGTCTAGTGACAAATTAGTGACAAAATCAAGCTGCTTTTA 357
QY 427 CAA 429
Db 358 TAA 360

RESULT 7
ABZ32493
ID ABZ32493 standard; DNA; 360 BP.
XX AC ABZ32493;
XX 30-JAN-2003 (first entry)
DE Candida albicans essential gene SEQ ID NO 6780.
XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; gene; ss.
XX Candida albicans.
XX WO200253728-A2.
XX 11-JUL-2002.
XX 26-DEC-2001; 2001WO-US049486.
XX 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX (ELIT-) ELITRA PHARM INC.
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
PI WPI; 2002-566694/60.
DR P-PSDB; ABP73943.
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.

```
XX Claim 37; SEQ ID NO 6780; 167pp + Sequence Listing; English.
PS The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungal
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of C. albicans cells and for
XX treating infection by C. albicans. The present sequence is that of an
XX essential Candida albicans gene used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office
SQ Sequence 360 BP; 129 A; 68 C; 62 G; 101 T; 0 U; 0 Other;

Query Match      20.68; Score 89; DB 6; Length 360;
Best Local Similarity 55.4%; Pred. No. 5.6e-15;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 67 AGAATTATTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCGAGGAACAGTTGCT 126
DB 10 ACATTATTACCAAGAGACTATTCAATACATCAACATGTTTCATCTCAAGTTAAGNAC 69

QY 127 CAGCTAAAGATCTGATGGCCAAAAGGAAGTGTTTGGTCAGCAAGACATCTGCCCT 186
DB 70 AAGGTGCAACAATTTGATCAAAACCAACACAGTTTTCATTGCTCCAAATCCTATTGTCCA 129

QY 187 TACTGTAAGCTACTTTGTCTACCTCTTCCAGAAATGGAAGTTCCTCAATCCAGGCC 246
DB 130 TACTGTAAGCTACCAAAAGCAC-----AATTGAAGCTATAACAAAGGATGCT 177

QY 247 CTGTGTGTGGAATTAGAATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAA 306
DB 178 TACATTTCTGATTAGAGAGTTGAGCAGCGTGTGAATCCAGNAGCATTTATTGGAA 237

QY 307 ATCTCGGGCCAAAACCTGACTTAAGCTATATACATCAATGGCAAGCACATTTGGTGAAC 366
DB 238 ATCACTGGTCAAGAACCGTTCCAAATGTCTTTATTGGTGGTCAACATATTGGTGGCAAT 297

QY 367 AGCGATTGTGAACCTTTGAGAAAAATGGCAAGTAGCTGAATATTTGAAGCCGGTATTT 426
DB 298 TCCGATGTGCAAGCTTTGAAGTCTAGTGACAAATTTAGATGACAAAATCAAAGCTGCTTTA 357

QY 427 CAA 429
DB 358 TAA 360

RESULT 8
ADRO2454
ID ADRO2454 standard; DNA; 621 BP.
XX
AC ADRO2454;
XX
DT
XX
XX 23-SEP-2004 (first entry)
XX
XX A. gossypii genomic DNA PAG1696UP.
```

```
XX Filamentous funghi; ds; forensic identification; gene characterisation;
KW intergenomic comparison; chromosome mapping.
XX
XX Eremothecium gossypii.
OS US6239264-B1.
XX
XX 29-MAY-2001.
PD
XX
XX 24-DEC-1997; 97US-00998416.
PF
XX
XX 31-DEC-1996; 97CH-00000016.
PR
XX
XX (SYNG-) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;
PI Knechtle P, Rebischung C;
XX
XX WPI; 1998-388120/33.
DR
XX
XX New gene for adenylate cyclase from Ashbya gossypii - useful for
PT generating recombinant microorganisms with alteration in gene of cAMP-
PT dependent signalling pathway for increasing production of fine chemicals.
XX
XX Example 3; SEQ ID NO 1146; 632pp; English.
PS
XX
XX The invention relates to isolated DNA molecules comprising isolated
CC genomic DNA sequences from the filamentous funghi Ashbya gossypii, the
CC sequences comprising ADR01309, ADR01366, ADR01367, ADR01388, ADR01428,
CC ADR01466, ADR01629, ADR01637, ADR02057, ADR02345 and ADR02369, chosen
CC from 1047 disclosed genomic sequences. Also included is a cloning vector
CC comprising a nucleotide sequence chosen from the above sequences. The
CC novel Ashbya gossypii genomic sequences are useful for forensic
CC identification, gene characterisation, for studying gene organisation by
CC intergenomic comparison (with Saccharomyces cerevisiae), identifying
CC biosynthetic genes for selectable markers, to isolate
CC promoters/terminators/centromeres, chromosome mapping, and in identifying
CC sequences unique to Ashbya gossypii for species identification. The
CC present sequence is an A. gossypii novel genomic sequence of the
CC invention.
XX
XX Sequence 621 BP; 137 A; 177 C; 179 G; 128 T; 0 U; 0 Other;

Query Match      15.0%; Score 64.6; DB 2; Length 621;
Best Local Similarity 55.0%; Pred. No. 5.4e-08;
Matches 149; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 100 AAAATGGTATCCAGGAACAGTTGCTACGTAAGGATCTGATGGCCAAAGGAAGTG 159
DB 350 ATAAATGGTTTCCCTTCGGTTATTAAACAGGTGCGCGCTAATCCAGCAGAACCGGTG 409

QY 160 TTTGTTGACGAGAAAGACATACCTGCTTACTGTAAGCTACTTTGTCTACCTCTTTCCAA 219
DB 410 TTCAATGTCATCAAGACGCTACTGTCCGTTATTCAGGCGGCAAGCGTACGTTGCTGGAG 469

QY 220 GAATTAAGCTTCCCAATCCAAAGCCCTTGTGTGGAATTAGATGAATAGCAATF--- 276
DB 470 GAGAAGCGCGTCCCGCAAGCGCAGTAAACCTGTTGGAGCTTGACACCATGGCGGAGGAG 529

QY 277 GGCTCAGAGATTCAGAGCGCTTTAGAGAAATCTCGGGCCAAAACCTGTACTTAACGTA 336
DB 530 GCGCGGCTGATCCAGCGCGCTTGCAGGAGCTGAGCGGCGAGCGCACCGTGGCCACATC 589

QY 337 TACATCAATGGCAAGCACATTTGGTGTAAACA 367
DB 590 TACATCAAGCGGCGCATGTTGGTGGCAACA 620

RESULT 9
ABZ53183
ID ABZ53183 standard; cDNA; 440 BP.
XX
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AC ABZ53183;
XX
XX 28-MAR-2003 (first entry)
XX
XX Aspergillus oryzae polynucleotide SEQ ID NO 2296.
XX
XX Aspergillus oryzae; fermentation; fungus; industrial; EST;
KW expressed sequence tag; gene; ss.
XX
XX Aspergillus oryzae.
XX
XX WO200279476-A1.
XX
XX 10-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-IB000890.
XX
XX 30-MAR-2001; 2001JP-00098371.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (NARE-) NAT RES INST BREWING.
XX (NORQ) NAT FOOD RES INST MIN AGRIC.
XX
XX Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
XX
XX WPI; 2003-046817/04.
XX
XX
XX Detection of expression of specific Aspergillus genes for monitoring the
PT fermentation and growth conditions of the fungus, using DNA probes.
XX
XX Claim 1; SEQ ID NO 2296; 48pp + Sequence Listing; Japanese.
XX
XX The invention relates to a polynucleotide having any of 6006 specific
CC sequences (ABZ5088-ABZ5693), which are expressed by a fungus under
CC specific culture conditions including one or more of eutrophic,
CC oligotrophic, solid, early germination, alkaline, high temperature, low
CC temperature or maltose culture or polynucleotides stringently hybridising
CC to these sequences. The polynucleotides are useful for monitoring the
CC progress of fermentation and the growth conditions of a fungus,
CC especially of Aspergillus oryzae which is widely used in industrial
CC fermentation. Also monitoring for fungal contamination. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 440 BP; 101 A; 139 C; 100 G; 100 T; 0 U; 0 Other;
SQ
Query Match 13.4%; Score 57.8; DB 8; Length 440;
Best Local Similarity 55.3%; Pred. No. 4.1e-06;
Matches 141; Conservative 0; Mismatches 102; Indels 12; Gaps 1;
Qy 134 AGGATCTGATTGGCCAAAGGAAGTGTGTGTCAGCAAGACATATCTGCCCTTACTGTGA 193
Db 103 AGGGCATCATCAAGCCCAAGCCGCTGCTGTTTCTTCCAAAGTCTACTGCCCTTACTGCA 162
Qy 194 AAGCTACTTTGTCTACCTCTTCCAAAGATTTGAAGCTTCCCAATCCAAAGCCCTTGTGT 253
Db 163 AATCTAGCAAGAGCCTCTCTTAGCCA-----GCTGGAGCAAGTACCTCACCA 210
Qy 254 TGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTTAGAAGAAATCTCGG 313
Db 211 TCGAGCTCGATGAAGAGCGGATGGCAGCGCCATCCAGGAGCCCTCGTGGAAATCAGCG 270
Qy 314 GCCAAAAAATGTACTTAACGTATATCATCAATGCGCAAGCAATTTGGTGGTAACAGCGATT 373
Db 271 GCCAGCGCACGCTCCCAACATTTTCATCAAGCAGAGCATATCGGTGGAAATCTCGGATC 330
Qy 374 TGGAAATTTTGAAGA 388
Db 331 TGCAGGCTCGCAAAA 345
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RESULT 10
ACL32590
ID ACL32590 standard; cDNA; 531 BP.
XX
XX ACL32590;
AC
XX 02-JUN-2005 (first entry)
DT
XX Rice abiotic stress response related polynucleotide SEQ ID NO:11153.
DE
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
XX
XX Oryza sativa.
OS
XX WO2003008540-A2.
PN
XX 30-JAN-2003.
PD
XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 24-AUG-2001; 2001US-0314662P.
PR
XX 26-SEP-2001; 2001US-0325277P.
PR
XX 21-NOV-2001; 2001US-0332132P.
PR
XX
XX (SVGN) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Disclosure; SEQ ID NO 11153; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 531 BP; 122 A; 111 C; 145 G; 153 T; 0 U; 0 Other;
SQ
Query Match 13.0%; Score 56; DB 11; Length 531;
Best Local Similarity 58.3%; Pred. No. 1.4e-05;
Matches 98; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 254 TGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAAGAAATCTCGG 313
Db 141 TTGAGTTGGACACTGGAAGCGATGGAATCAGATTCAGTCAGCTCTTGCTGAATGGACTG 200
Qy 314 GCCAAAAAATGTACTTAACGTATATCATCAATGCGCAAGCAATTTGGTGGTAACAGCGATT 373
Db 201 GGCAGAGGAGCTGTTCGCAATGTCTTCATCAATGGAAAAACACATTTGGTGGCTGTGACGATA 260
Qy 374 TGGAAATTTTGAAGAAAAATGGCAAGTCTAGCTGAATATTTTGAAGCCGG 421
Db 261 CTATTGCACTGAACAAGGGAGGGAAGCTGTTGCTCTGCTGACGGAGG 308
```

RESULT 11

ADK90702
ID ADK90702 standard; cDNA; 733 BP.

XX AC
XX ADK90702;

XX AC
XX 20-MAY-2004 (first entry)

XX DE
XX Rice oxidoreductase stress-related protein cDNA OZ1116C2194 SeqID 47.

XX KW rice; gene; ss; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thioredoxin; THX; Quantitative trait Locus; QTL.

XX OS
XX Oryza sativa.

XX PN
XX WO2004018687-A2.

XX XX
XX 04-MAR-2004.

XX XX
XX 01-JUL-2003; 2003WO-EP006994.

XX XX
XX 07-AUG-2002; 2002EP-00017671.

XX XX
XX (BADI) BASF PLANT SCI GMBH.

XX XX
XX Chardonnais A, Puzio P;

XX PI
XX WPI; 2004-226856/21.

XX DR
XX P-PSDB; ADK90703.

XX PT
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.

XX PS
XX Claim 5; SEQ ID NO 47; 140pp; English.

XX CC This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polynucleotide
CC sequence is a rice ORSRP cDNA of the invention.

XX SQ
XX Sequence 733 BP; 222 A; 176 C; 166 G; 169 T; 0 U; 0 Other;

Query Match 12.9%; Score 55.6; DB 12; Length 733;
Best Local Similarity 60.7%; Pred. No. 2e-05;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 254 TGGAACTAGTAAGTAAATGGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAATCTCGG 313

Db 258 TTGAGTTGGATGGGGAGTGATGGATCTGAGCTGCAGCTCGGCACCTTGCTGAATGACTG 317

QY 314 GCCAAAAAAGCTACCTAAAGTATACATCAATGGCAAGCACATTTGGTGGTAACAGCGATT 373

Db 318 GACAAAGGACTGTTCNAATGTCTTCATCAATGGGAAGCATATTTGGTGGCTGTGATGATA 377

QY 374 TGGAACTTTGAAGAAAAATGGCAAGTTAG 403

Db 378 CTTTGGCATTGAACAAATGAAGGGAAGCTGG 407

RESULT 12

AAC43844
ID AAC43844 standard; DNA; 619 BP.

XX AC
XX AAC43844;

XX DT
XX 18-OCT-2000 (first entry)

XX DE
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 40715.

XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX OS
XX Arabidopsis thaliana.

XX PN
XX EP1033405-A2.

XX PD
XX 06-SEP-2000.

XX XX
XX 25-FEB-2000; 2000EP-00301439.

XX XX
XX 25-FEB-1999; 99US-0121825P.

XX PR
XX 05-MAR-1999; 99US-0123180P.

XX PR
XX 09-MAR-1999; 99US-0123548P.

XX PR
XX 23-MAR-1999; 99US-0125788P.

XX PR
XX 23-MAR-1999; 99US-0126264P.

XX PR
XX 29-MAR-1999; 99US-0126785P.

XX PR
XX 01-APR-1999; 99US-0127462P.

XX PR
XX 08-APR-1999; 99US-0128234P.

XX PR
XX 16-APR-1999; 99US-0128714P.

XX PR
XX 16-APR-1999; 99US-0129845P.

XX PR
XX 19-APR-1999; 99US-0130077P.

XX PR
XX 21-APR-1999; 99US-0130449P.

XX PR
XX 23-APR-1999; 99US-0130510P.

XX PR
XX 28-APR-1999; 99US-0130891P.

XX PR
XX 30-APR-1999; 99US-0131449P.

XX PR
XX 30-APR-1999; 99US-0132048P.

XX PR
XX 04-MAY-1999; 99US-0132407P.

XX PR
XX 05-MAY-1999; 99US-0132484P.

XX PR
XX 06-MAY-1999; 99US-0132485P.

XX PR
XX 06-MAY-1999; 99US-0132486P.

XX PR
XX 07-MAY-1999; 99US-0132487P.

XX PR
XX 11-MAY-1999; 99US-0132863P.

XX PR
XX 14-MAY-1999; 99US-0134256P.

XX PR
XX 14-MAY-1999; 99US-0134218P.

XX PR
XX 14-MAY-1999; 99US-0134219P.

XX PR
XX 14-MAY-1999; 99US-0134370P.

XX PR
XX 18-MAY-1999; 99US-0134370P.

XX PR
XX 19-MAY-1999; 99US-0134768P.

XX PR
XX 20-MAY-1999; 99US-0134941P.

XX PR
XX 21-MAY-1999; 99US-0135124P.

XX PR
XX 24-MAY-1999; 99US-0135299P.

XX PR
XX 25-MAY-1999; 99US-0136021P.

XX PR
XX 27-MAY-1999; 99US-0136392P.

XX PR
XX 28-MAY-1999; 99US-0136782P.

XX PR
XX 01-JUN-1999; 99US-0137222P.

XX PR
XX 03-JUN-1999; 99US-0137528P.

XX PR
XX 04-JUN-1999; 99US-0137502P.

XX PR
XX 07-JUN-1999; 99US-0137724P.

XX PR
XX 08-JUN-1999; 99US-0138094P.

XX PR
XX 10-JUN-1999; 99US-0138540P.

XX PR
XX 10-JUN-1999; 99US-0138847P.

XX PR
XX 14-JUN-1999; 99US-0139119P.

XX PR
XX 16-JUN-1999; 99US-0139452P.

XX PR
XX 16-JUN-1999; 99US-0139453P.

XX PR
XX 17-JUN-1999; 99US-0139492P.

XX PR
XX 18-JUN-1999; 99US-0139454P.

XX PR
XX 18-JUN-1999; 99US-0139455P.

XX PR
XX 18-JUN-1999; 99US-0139456P.

XX PR
XX 18-JUN-1999; 99US-0139457P.

XX PR
XX 18-JUN-1999; 99US-0139458P.

XX PR
XX 18-JUN-1999; 99US-0139459P.


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PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 08-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
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PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
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Query Match 12.8%; Score 55.2; DB 3; Length 619;

Best Local Similarity 58.5%; Pred. No. 2.5e-05; Mismatches 68; Indels 0; Gaps 0;

Matches 96; Conservative 0;

QY 250 GTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATC 309

Db 269 GTACTTGAGCTCGATGAATGAGTGGAGGTGAGATCCCAATCAGCTTTATCAGAGTGG 328

QY 310 TCGGGCAAAAACCTGTACTTAACGTATACATCAATGGCAGCACATTTGGTGTAAACAGC 369

Db 329 ACTGGACAGACCAACAGTTCCAAACGCTTCATCAAGGAAACACATCGGTGGATCGCAT 388

QY 370 GATTTCGAACTTTTGAAGAAATGCAAGTTAGCTGAAATATT 413

Db 389 AGAGTGTGAGAGACCAACAGCAAGCAAGCTTTGTACTCTATT 432

RESULT 13

AD570498
ID AD570498 standard; cDNA; 278 BP.
XX
AC AD570498;
XX
DT 18-NOV-2004 (first entry)
XX
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 5514.
XX
KW Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
KW seed development; disease resistance; insect infestation; fungal disease;
KW bacterial infection; Goss' Bacterial Wilt; blight; bacterial leaf blight;
KW Stewart's Bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;
KW bacterial stripe; maize dwarf mosaic virus infection;
KW environmental stress; water stress; pH stress; temperature stress;
KW pollution; injury; pesticide.
XX
OS Zea mays.
XX
PN US2003237110-A9.
XX
PD 25-DEC-2003.
XX
PF 06-AUG-2001; 2001US-00923876.
XX
PR 12-MAY-1998; 98US-0085331P.
PR 21-APR-1999; 99US-00298329.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lalgudi RV, Ito LY, Sherman BK;
PI WPI; 2002-195165/25.
DR
XX New corn seedling-derived polynucleotides and polypeptides, useful in
PT identifying and altering desired characteristics associated with growth
PT and development, disease resistance, environmental adaptability, quality
PT and yield.
XX
PS Claim 1; SEQ ID NO 5514; 33pp; English.
XX
XX The invention relates to a corn seedling-derived polynucleotide (cdp)
CC selected from ADS64985-ADS71316, or their complements and fragments. Also
CC included are a composition for the detection of altered expression of a
CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
CC method of detecting a polynucleotide in a biological sample using a cdp,
CC a method for using oligomers (and amplification) to recover a regulatory
CC element from a DNA library using oligomers designed against a cdp, a
CC seedling specific regulatory element that regulates the expression of a
CC cdp, an expression vector containing a cdp or regulatory element, a plant
CC transformed with the vector, a host cell containing the vector (and
CC identifying a compound which binds a CDP and screening a plurality of
CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,
CC proteins, vectors, cells and antibodies are useful for the
CC identification, evaluation and alteration of seed growth and development,
CC disease resistance (e.g. to insect infestation, fungal disease, bacterial
CC infection, Goss' Bacterial Wilt, blight, Stewart's Bacterial Wilt, Holcus
CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
CC mosaic virus infection) and resistance to environmental stress (e.g.
CC water stress, pH stress, temperature stress, pollution, injury or
CC pesticides. The present sequence is cdp cDNA sequence.
XX
SQ Sequence 278 BP; 74 A; 56 C; 77 G; 71 T; 0 U; 0 Other;

Query Match 12.7%; Score 55; DB 7; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.2e-05;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 242 AGGCCCTGTGTGGATTAGATGAAATGAGCAATGCTCAGAGATTCAAGAGCGCTTTAG 301
DB 77 AGCCATATGTTGGAGCTTGATCAGGAGGAGATGCTCAGAGATTCAGATGCCTTAC 136

QY 302 AAGAAATCTCGGGCCAAAAAACTGTACCTAAGTATACATCAATGCAAGCATTGGTG 361
DB 137 TTGAGATAGTTGGCAGCGGTACTGTGCTCCCTCAAGTTTTTGTCCATGGAAGCACCTGGTG 196
QY 362 GTAACAGCGATTGTGAAACTTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAA 416
DB 197 GTTCTGACGATCTGTTGACTCTCTACGAAAGTGGAAAACTGGCTAGACTTCTAAA 251

RESULT 14

AE65134
ID AE65134 standard; DNA; 392 BP.
XX
AC AE65134;
XX
DT 22-SEP-2005 (first entry)
XX
DE Rice genome derived DNA sequence, SEQ ID 279.
XX
KW transcription; gene regulation; transgenic plant; RNA interference;
KW transformation; antibody; ds.
XX
OS Oryza sp.
XX
PN JP2005185101-A.
XX
PD 14-JUL-2005.
XX
PF 11-DEC-2002; 2002JP-00383870.
XX
PR 30-MAY-2002; 2002JP-00203269.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
XX
PI Kikuchi H, Hayashizaki Y, Otomo Y, Matsubara K, Murakami K;
PI Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M;
PI Doi K, Kawai J;
XX
WPI; 2005-566181/58.

Novel DNA encoding transcription factor, derived from rice plant, useful
PT for obtaining transcriptional-regulatory regions in plant and for
PT producing modified plant.
XX
PS Claim 1; SEQ ID NO 279; 2928pp; Japanese.
XX
XX The invention relates to a novel DNA sequence encoding a transcription
CC factor derived from a plant. The invention further comprises antisense
CC RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,
CC transformed plant cells, antibodies and proteins, all related to the
CC novel plant DNA sequences of the invention. The novel DNA is preferably
CC derived from a rice-genome database. The invention further provides a
CC method for determining the transcription regulatory regions of the rice
CC genome. The novel DNA is useful for controlling the expression of a gene
CC in a plant and for producing a modified plant with desired and different
CC characteristics. The plant DNA and method enables the acquisition of many
CC transcriptional-regulatory regions. This polynucleotide represents a DNA
CC sequence taken from a rice genome clone library for use in the invention.
CC Note: This sequence is not shown in the specification. It has been
CC retrieved from a sequence listing in electronic format from the Japanese
CC Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to
CC 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791,
CC however, the sequence listing only provided the DNA sequences of SEQ ID
CC Nos 1 to 3032.

Sequence 392 BP; 112 A; 75 C; 91 G; 114 T; 0 U; 0 Other;
Query Match 12.7%; Score 55; DB 14; Length 392;
Best Local Similarity 57.1%; Pred. No. 2.5e-05;

[illegible]

RESULT 15

ADK90700

ID ADK90700 standard; cDNA; 628 BP.

AC ADK90700;

DT 20-MAY-2004 (first entry)

DE Rice oxidoreductase stress-related protein cDNA OZ1116C12744 SeqID 45.

rice; gene; ss; transgenic; abiotic stress response; crop plant;
KW oxalodihydroxyacid decarboxylase; oxalate decarboxylase;
KW oxalodihydroxyacid decarboxylase; oxalate decarboxylase;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thiorredoxin; TRX; Quantitative Trait Locus; QTL.

OS. *Oryza sativa*.

PN WO2004018687-A2.

04-MAR-2004.

01-JUL-2003: 2003WO-EP006994.

07-AUG-2002: 2002EP-00017671.

PA (BADI) BASF PLANT SCI GMBH.

Chardonnais A. Puzio P:

WPI: 2004-226856/21.

UK P-PSUB; ADK90701.
XX

New transgenic plant cell transformed by oxidoreductase stress-related protein (ORSRP) coding nucleic acid, useful for producing a transgenic plant with increased environmental stress tolerance.

PS Claim 5; SEO ID NO 45; 140pp; English.

This invention relates to novel transgenic plant cells transformed by genes encoding proteins associated with the abiotic stress response. Specifically, it refers to transgenic crop plants expressing the heterologous oxidoreductase stress-related protein (ORSRP) that confers increased tolerance and/ or resistance to environmental stresses such as salinity, drought, temperature, chemicals or pathogens. The present invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or thioredoxin (TRX) proteins, where expression is under the control of an inducible tissue-specific or developmentally-specific promoter and furthermore it provides antisense oligos and RNA interference molecules to inhibit ORSRP expression. In addition, these nucleic acids are useful as Quantitative Trait Locus (QTL) markers that can map genetic loci associated with environmental stress tolerance. This polynucleotide sequence is a rice ORSRP cDNA of the invention.

Sequence 628 BP: 133 A; 166 C; 164 G; 165 T; 0 U; 0 Other;

Query Match	12.7%	Score 55;	DB 12;	Length 628;
Best Local Similarity	57.1%	Pred. No. 2.9e-05;		
Matches 100;	Conservative	0;	Mismatches 75;	Indels 0;
				Gaps 0;

242	AGGCCCTTGTTGGATTAGATGAATGACCAATGCTCAGAGATTCAAGACGCTT	301
311	AGCCGTATGTTGGAGCTTGATCAGCAGAGATGTTGGAGATTGAGATGGCTTAT	370
302	AAGAAATCTCGGGCCAAAAAACTGTACTTAACGTATACATCAATGGCAGCA	361
371	CTGACATGGTTGGCAGCGCACTGTTCTCAAGTTTTTGTCCATGGGAAGCAC	430
362	GTAAACAGCGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAATATT	416
431	GCTCTGATGATCTGTTGAAGCATATGAGAGTGGCAAGCTAGCCAACTTTTGA	485

Search completed: November 7, 2006, 03:38:57
Job time : 456 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:33:13 ; Search time 4440 Seconds
(without alignments)

5440.800 Million cell updates/sec

Title: US-10-523-362-3

Perfect score: 432

Sequence: 1 atggagaccaatttttcctt.....tgaagccgtatttcaatag 432

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346.8	80.3	969	14	CNS06HAM
C 2	241.8	56.0	390	10	T36608
C 3	221	51.2	307	10	T36930
C 4	164	38.0	902	14	CNS06KVC
5	137.6	31.9	920	14	CNS075L8
6	137.6	31.9	997	14	CNS073AT
7	124.6	28.8	966	14	CNS075E3
C 8	99.6	23.1	434	11	AZ925612
C 9	94	21.8	420	10	T37408
C 10	90.6	21.0	454	11	AZ926128
C 11	72.4	16.8	848	13	CZ286838
C 12	68.8	15.9	492	9	DN156309
C 13	68.4	15.8	529	8	CN813116
C 14	68	15.7	522	8	CN813785
C 15	67.6	15.6	477	5	CD459632
C 16	66.6	15.4	504	9	DN156705
C 17	66.4	15.4	772	13	CZ289630
C 18	66	15.3	405	3	BP520191
C 19	66	15.3	435	3	BP520391

20	66	15.3	762	8	CV182757
C 21	65.2	15.1	381	2	BJ955512
C 22	65.2	15.1	388	2	BJ953571
C 23	65.2	15.1	433	2	BJ942895
C 24	65.2	15.1	435	2	BJ953134
C 25	65.2	15.1	452	5	CD457966
C 26	65.2	15.1	472	2	BJ942458
C 27	65.2	15.1	501	2	BJ961669
C 28	65.2	15.1	526	2	BJ950022
C 29	65.2	15.1	532	2	BJ950704
C 30	65.2	15.1	548	2	BJ167220
C 31	65.2	15.1	548	2	BJ950490
C 32	65.2	15.1	552	2	BJ950702
C 33	65.2	15.1	559	2	BJ941223
C 34	65	15.0	433	3	BP508298
C 35	63.6	14.7	583	8	CO214935
C 36	63.2	14.6	586	8	CO208264
C 37	63.2	14.6	783	1	AL669647
C 38	63	14.6	405	2	BJ944737
C 39	63	14.6	477	8	CN811635
C 40	61.4	14.2	272	2	BJ961436
C 41	61.4	14.2	332	2	BJ961671
C 42	61.4	14.2	368	2	BJ960957
C 43	61.4	14.2	372	2	BJ951802
C 44	60.6	14.0	657	5	CF867737
C 45	60.6	14.0	779	4	CB897783

ALIGNMENTS

RESULT 1
CNS06HAM

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS06HAM 969 bp DNA linear GSS 17-AUG-2005
T7 end of clone AS0AA011A12 of library AS0AA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.

AL398756

AL398756.1 GI:12152529

GSS.

Saccharomyces uvarum

Saccharomyces uvarum

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

1 (bases 1 to 969)

Souciot J., Aigle M., Artiguenave F., Blandin G.,

Bolotin-Fukuhara M., Bon E., Brottier P., Casaregola S., de

Montigny J., Dujon B., Durand P., Gaillardin C., Lepingle A.,

Llorente B., Malpertuy A., Neuvéglise C., Ozier-Kalogeropoulos O.,

Potier S., Saurin W., Tekai F., Toffano-Nioche C.,

Wesolowski-Louvel M., Wincker P., and Weissenbach J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)

11152876

2 (bases 1 to 969)

Bon E., Neuvéglise C., Casaregola S., Artiguenave F., Wincker P.,

Aigle M. and Durand P.

Genomic exploration of the hemiascomycetous yeasts: 5.

Saccharomyces bayanus var. uvarum

FEBS Lett. 487 (1), 37-41 (2000)

11152880

3 (bases 1 to 969)

Genoscope.

Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomycetes

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Contact: Weinstock,K. and Venter,J.C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13-21.

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FEATURES
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Qy 208 ACCCTCTTCCAAGAAATTGAACGTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAA 267
Db 307 ACCCTCTTCCAAGAAATTGAACGTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAA 248

Qy 268 ATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGAAATCTCGGCCCAAAAACGTGA 327
Db 247 ATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGAAATCTCGGCCCAAAAACGTGA 188

Qy 328 CCTAACGTATACATCAATGCAAGCACATTGGTGTAAACAGCGATTTGGAACCTTTGAAG 387
Db 187 CCTAACGTATACATCAATGCAAGCACATTGGTGTAAACAGCGATTTGGAACCTTTGNAG 128

Qy 388 AAAAAATGGCAAGTTAGCTGAATATTTGAAGCCGCTATTTCAATAG 432
Db 127 NAAATGGCAAGTTAGTGNATATTTGAAGCCGCTATTTCAATAG 83

RESULT 4
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LOCUS T7 end of clone ATOAA009A07 of library ATOAA from strain CBS 4311
DEFINITION of Saccharomyces servazzii, genomic survey sequence.
ACCESSION AL403498
VERSION AL403498.1 GI:12163814
KEYWORDS GSS.
SOURCE Saccharomyces servazzii
ORGANISM Saccharomyces servazzii
REFERENCE 1 (bases 1 to 902)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FBES Lett. 487 (1), 3-12 (2000)
11152876
2 (bases 1 to 902)
Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H.,
Artiguenave,F., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 7.
Saccharomyces servazzii
FBES Lett. 487 (1), 47-51 (2000)
11152882
3 (bases 1 to 902)
Genoscope.

```

```

TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
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      /clone_lib="ATOAA"
      /note="end : T7"
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    complement(<153..>503)
    /inference="non-experimental evidence, no additional
    details recorded"
    /note="similar to Saccharomyces cerevisiae ORF YDR513w [
    TFR1 ; glutaredoxin ]"
  ORIGIN
    Query Match      38.0%; Score 164; DB 14; Length 902;
    Best Local Similarity 66.3%; Pred. No. 6.7e-34;
    Matches 236; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

Qy 77 CTAAGAAGATTTTATCTACTCCAAAATGTTATCCAGGAACAGTGTCTCAGTAAGG 136
Db 499 CTAACAAATTTTATTTACTCACAAAATGTTCTCTCAAGCTACTATCAACCGTCAAG 440

Qy 137 ATCTGATTGGCCAAAGGAAGTGTGTTGTCAGCAAGACATCTGCGCTTACTGTAAAG 196
Db 439 AATTAAATGCTGAAGAGATATTTTCATTCCTTCAAGACTTACTGTCCATCTGCTG 380

Qy 197 CTACTTTGTCTACCTCTTCCAAAGAAATGAACGTTCCCAATCCAAAGGCCCTTGTGTGG 256
Db 379 CCACCTTTAAGACTGTGTTCAAGAGACCTTAACGCTCCCTGAATCCAAAGCTGCTGTGTTAC 320

Qy 257 AATTAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAGAAATCTCGGGCC 316
Db 319 AATTAGATGAATGAGTATGATGGTGGCCGAAATTCAGAAGCTTTGAAGGAAATTTACTGGTC 260

Qy 317 AAAAAACTGTACCTTAACGTATACATCAATGGCAAGCACATGTTGTTGTAACAGCGATTGG 376
Db 259 AATCTACCGTCCCAAAACACTTTTCATTAACGCTCAACATGTTGTTGTAATGACAATCTAC 200

Qy 377 AAACCTTTGAAGAAAAATGGCAAGTTAGCTGAATATTTGAAGCCGCTATTTCAATAG 432
Db 199 AAACCTTTGAAGAACTCTGTTAGCTAGACTCTTTTATTAAGGATGCTCTTAGCTTAG 144

RESULT 5
CNS075L8 920 bp DNA linear GSS 07-JUL-2001
LOCUS clone BA0AB036E06 of library BA0AB from strain CLIB 210 of
DEFINITION Kluyveromyces lactis, genomic survey sequence.
ACCESSION AL430242
VERSION AL430242.1 GI:12213436
KEYWORDS GSS.
SOURCE Kluyveromyces lactis
ORGANISM Kluyveromyces lactis
REFERENCE 1 (bases 1 to 920)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

```

Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Maupertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, P., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissbach, J.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL
PUBMED
11152876

REFERENCE
2 (bases 1 to 920)
Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R., Robert, C., Ternier, M., Wincker, P. and Wesolowski-Louvel, M.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 11.

JOURNAL
PUBMED
11152886

REFERENCE
3 (bases 1 to 920)
Genoscope.

TITLE
Direct Submission

JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Creneau, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
1..920
/organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/strain="CLIB 210"
/variety="lactis"
/db_xref="taxon:28985"
/clone="BA0AB036E06"
/clone_lib="BA0AB"
/447..>806
/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 ; Glutaredoxin]"

misc_feature
447..>806
/inference="non-experimental evidence, no additional details recorded"

misc_feature
513..>806
/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YCL035c [GRX1 ; Glutaredoxin]"

ORIGIN

Query Match 31.9%; Score 137.6; DB 14; Length 920;
Best Local Similarity 63.1%; Pred. No. 1.2e-26;
Matches 212; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 89 TATCTACTCCAAAATGGTATCCAGGAAACAGTTGCTACGTAAGGATCTGATGGCC 148
DB 499 TACATCTTTCAAAATGCCAAGTGGCGCAACATGCTGTGTCACAGGTTTAACTCACT 558
QY 149 AAAAGGAAGTGTGTGTGGACGAAAGACATACCTGCCCTTACTGTAAGCTACTTGTCTA 208
DB 559 CATCTAAGATCTTTGTCGTTTCAAGAGACATCTGTCATCTGCCAAGCCACTTTGAAA 618
QY 209 CCCTCTCCAGAAATGAAGTTCCTCCAAATCCAGGCCCTTGTGTGGAATTAGATGAA 268
DB 619 CTTTGTGTTGAAGAAAGAAAGGTGGACAAAAGTTGGCTACTGTTTTCGAATTGAACCAAC 678
QY 269 TGAGCAATGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGGGCCAAAACCTGTAC 328
DB 679 TAGAAGATGTTTCGATATTCAGATGCTTTTGCAGAAATATCCGGCCAAAAGACTGTTTC 738

QY 329 CTAACGTATACATCAATGCGACAGCATTTGGTGGTAACGCGATTTGGAACCTTGAAGA 398
DB 739 CAAACATCTTTTAAATTAATGGCAAGCACATCGGTGGTAACCTCTGATTTGCAAGAGTTGAACA 798

QY 389 AAAATGGCAAGTTAGCTGAATATTTGAAGCCGGTAT 424
DB 799 ACTCCGGTGATTGGATAAGTTGTTGGCTTCCTTAT 834

RESULT 6
CNS073AT 997 bp DNA linear GSS 07-JUL-2001
clone BA0AB018B12 of library BA0AB from strain CLIB 210 of Kluyveromyces lactis, genomic survey sequence.

ACCESSION
AL427275

VERSION
AL427275.1 GI:12210469

KEYWORDS
GSS.

SOURCE
Kluyveromyces lactis

ORGANISM
Kluyveromyces lactis

REFERENCE
1 (bases 1 to 997)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Maupertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, P., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissbach, J.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL
PUBMED
11152876

REFERENCE
2 (bases 1 to 997)
Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R., Robert, C., Ternier, M., Wincker, P. and Wesolowski-Louvel, M.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 11.

JOURNAL
PUBMED
11152886

REFERENCE
3 (bases 1 to 997)
Genoscope.

TITLE
Direct Submission

JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Creneau, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
Location/Qualifiers
1..997
/organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/strain="CLIB 210"
/variety="lactis"
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/clone_lib="BA0AB"
/563..>922
/inference="non-experimental evidence, no additional details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 ; Glutaredoxin]"
/inference="non-experimental evidence, no additional details recorded"

misc_feature
563..>922
/inference="non-experimental evidence, no additional details recorded"

misc_feature
629..>922
/inference="non-experimental evidence, no additional details recorded"

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
1..966
/organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/strain="CLIB 210"
/variety="lactis"
/db_xref="taxon:28985"
/clone="BA0AB035A08"
/clone_lib="BA0AB"
misc_feature
1..5240
/inference="non-experimental evidence, no additional details recorded"
/notes="similar to Saccharomyces cerevisiae ORF YCL035c [GRX1 : glutaredoxin]"
similar to Saccharomyces cerevisiae ORF YDR513w [TTR1 : glutaredoxin]"

ORIGIN

Query Match 28.8%; Score 124.6; DB 14; Length 966;
Best Local Similarity 66.7%; Pred. No. 4.7e-23;
Matches 178; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 158 TGTGTTGTCAGCAAGACATCTGCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCC 217
DB 2 TCTTTGTCGCTTCAAGACATCTGCTTACTGCTTCAAGCCACTTTGAAACCTTTGTTG 61
QY 218 AAGAATTGAACGTTCCCAATCCAGCCCTTGTGTGGTAATTAGATGAATAGCAATG 277
DB 62 AAGAAAGAGAGGTGGCAAAAAGTTGGCTACTCTTTTGCATTTGAAACCACTAGAAGATG 121
QY 278 GCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGGCCCAAAAACCTGTACCTAACCTAT 337
DB 122 GTTCCGATATTCAGGATGCTTTGGCAGAAATTAACCGCCAAAAGACTGTTCCAAACATCT 181
QY 338 ACATCAATGCGCAAGCACATTTGGTGGTAACGCAATTTGGAACCTTTGAAGAAAAATGGCA 397
DB 182 TTATTAATGCGCAAGCACATCGGTGGTAACTCTGATTTGCAAGAGTTGAACCACTCCGGTG 241
QY 398 AGTTAGCTGAATATTGAAGCCGGTAT 424
DB 242 ATTTGGATAAGTTGTTGGCTTCCTTAT 268

RESULT 8

AZ925612/c
LOCUS
DEFINITION
genomic clone 4910.ez34c13.s1 Saccharomyces paradoxus N17 Saccharomyces paradoxus
AZ925612
ACCESSION
AZ925612.1 GI:13496512
KEYWORDS
GSS.
SOURCE
Saccharomyces paradoxus
ORGANISM
Saccharomyces paradoxus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE
AUTHORS
Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H., and Johnston, M.
TITLE
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
JOURNAL
Unpublished (2001)
COMMENT
Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA

details recorded"
/note="similar to Saccharomyces cerevisiae ORF YCL035c [GRX1 : glutaredoxin]"

Query Match 31.9%; Score 137.6; DB 14; Length 997;
Best Local Similarity 63.1%; Pred. No. 1.3e-26;
Matches 212; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
QY 89 TATCTACTCCAAATGGTATCCCGAGCAAGTGTCTCAGTAAAGGATCTGATGGCC 148
DB 615 TACATCTTTCAAATGCCAGTCCGCAACATCGCTCGTGTCCAAAGGTTTATCAACT 674
QY 149 AAAAGGAAGTGTGTTGTCAGCAAGACATCTGCTTACTGTAAAGCTACTTTGTCTA 208
DB 675 CATCTAAGATCTTGTGCTTCAAGACATCTGCTCATCTGCAAGCCACITTTGAAA 734
QY 209 CCCTCTTCCAAAGATTGAAGTTCCTCCAAATCCAAAGGCTTGTGTGGAATTAGATGAA 268
DB 735 CTTTGTGTTGAAGAAAAGAGGTGACAAAAGTTGGCTACTGTTTTCGAATTGAACCAAC 794
QY 269 TGAGCAATGCTCAGAGATTCAGACGCTTTAGAGAAATCTCGGCCCAAAAACCTGTAC 328
DB 795 TAGAAGATGTTCCGATATTACAGATGCTTTGGCAGAAATTAACCGCCAAAAGACTGTC 854
QY 329 CTAACGTATACATCAATGGCAAGCACATTTGGTGTAAACAGGATTTGGAAACTTTGAAGA 388
DB 855 CAACATCTTTAATGTCGCAAGCACATCGGTGTACTCTGATTTGCAAGATTGAACA 914
QY 389 AAAATGGCAATGTTAGCTGAAATATTGAAGCCGGTAT 424
DB 915 ACTCCGGTATTGGATAAGTTGTTGGCTTCCTTAT 950

RESULT 7

CNS075E3
LOCUS
DEFINITION
clone BA0AB035A08 of library BA0AB from strain CLIB 210 of
Kluyveromyces lactis, genomic survey sequence.
AL429985
ACCESSION
AL429985.1 GI:12213179
KEYWORDS
GSS.
SOURCE
Kluyveromyces lactis
ORGANISM
Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetaceae; Saccharomycetaceae; Kluyveromyces.
REFERENCE
AUTHORS
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Caesaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL
PES Lett. 487 (1), 3-12 (2000)
PUBMED
11152876
REFERENCE
AUTHORS
2 (bases 1 to 966)
Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmesse, R., Montrocher, R., Robert, C., Ternier, M., Wincker, P. and Wesolowski-Louvel, M.
TITLE
Genomic exploration of the hemiascomycetous yeasts: 11.
JOURNAL
FEMS Lett. 487 (1), 66-70 (2000)
PUBMED
11152886
REFERENCE
AUTHORS
3 (bases 1 to 966)
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

Tel: 314 362 2735
 Fax: 314 362 7855
 Email: mj@genetics.wustl.edu
 Class: random plasmid subclone.
 Location/Qualifiers

FEATURES

source
 1..434
 /organism="Saccharomyces paradoxus"
 /mol_type="genomic DNA"
 /strain="N17"
 /db_xref="taxon:27291"
 /clone="4910.e234c13.81"
 /clone_lib="Saccharomyces paradoxus N17"
 /note="Random genomic sequence"

ORIGIN

Query Match 23.1%; Score 99.6; DB 11; Length 434;
 Best Local Similarity 64.6%; Pred. No. 2.9e-16;
 Matches 164; Conservative 0; Mismatches 89; Indels 1; Gaps 1;
 QY 64 ACAAGAATTATGCTAAAGATTTTATCTACTCCAAAATGATGATCCCA-GGAAACAGT 122
 DB 254 ATACAATAATACAAACATCTTAGAAGAGAAAAAATGATGATCCCATAGAACTAT 195
 QY 123 TGCTCAGTAAAGATCTGATGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATACG 182
 DB 194 TAAACAGTTAAGACCTATTGAGAGAAAGAGATCTTTGTTGCATCCAAAACGTACTG 135
 QY 183 CCCTTACTGTAAGCTACTTTGTCTACCTCTTCCAAAGATTTGAACGTTCCCAATCCAA 242
 DB 134 CCATAGTGCATGAGCTCTAAACAGCGCTTTTCGAGAGCTGAAGTTCCAAAGTCCAA 75
 QY 243 GGCCCTGTGTTGAATTAGATGAATGACATGCTCAGAGATTCAAGACGCTTTAGA 302
 DB 74 AGTTTGTGTTTGCATTTGAATGAACGAGATGAAGGATGGCGCAGACATTCAAGCGCGTTACA 15
 QY 303 AGAAATCTCGGGC 316
 DB 14 TGAGATTATGGCC 1

RESULT 9
 T37408/c
 LOCUS 420 bp mRNA linear EST 11-JAN-1995
 DEFINITION EST02526 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae
 cDNA 3' end, mRNA sequence.
 T37408
 T37408.1 GI:621225
 EST.
 Saccharomyces cerevisiae (baker's yeast)
 Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 1 (bases 1 to 420)
 Weinstock, K.
 Saccharomyces cerevisiae cDNAs
 Unpublished (1995)
 Contact: Weinstock, K. and Venter, J.C.
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@db.tigr.org
 For clone availability please contact the TIGR Database
 (tdbinfo@db.tigr.org)

FEATURES

source
 1..420
 /organism="Saccharomyces cerevisiae"
 /mol_type="mRNA"
 /strain="X2180-1A"
 /db_xref="taxon:4932"
 /clone_lib="S. cerevisiae strain X2180-1A"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 Seq primer: M13-21.
 Location/Qualifiers

FEATURES

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 Seq primer: M13-21.
 Location/Qualifiers

ORIGIN

Query Match 21.8%; Score 94; DB 10; Length 420;
 Best Local Similarity 61.0%; Pred. No. 1e-14;
 Matches 183; Conservative 0; Mismatches 114; Indels 3; Gaps 2;
 QY 135 GGATCTGATTGCCCAAGGAAGTGTGTTGTCACCAAGACATACG-CCCTTACTGTA 193
 DB 420 GGACCCCTATTGCGAGAAACGAGATCCTCGTCGATCCAAACCGTACTGCCCCATCTGCC 361
 QY 194 AAGCTACTTTGTCTACCTCTTCCAAAGATTTGAAGGTTCCCAAGGCTCCCAAGTCTCGT 251
 DB 360 ATGCGCCCTTAAACACGCTTTTGAAGGTTTAAAGGTTCCCAAGGCTCCCAAGTCTCGT 301
 QY 252 GTTGAATTAGATAAATGAGCAATGGCTCAGAGATTTCAAGACGCTTTAGAGAAATCTC 311
 DB 300 TTTCGNATTGAATGACATGAAGGAAGGCGCAGACATTCAGGCTGCGTTATATGAGATTAA 241
 QY 312 GGGCCAAAACCTGATACCTTAAGCTATACATCAATGCGAAGCACATTTGGTGGTAACAGCGA 371
 DB 240 TGGCCAAAAGAACCGTGCCCAACATCTATATTAAATGTTAAACATATTGGAGGCAACGACCA 181
 QY 372 TTTGGAACCTTTGAAGAAAAATGCGAAGTTAGCTGAAATATTGAAGCCGCTATTTCATATA 431
 DB 180 CTTGCGNGGNAATTGAGGAGACTGGTGAATTGGAGGNATTGTTAGAACCTATTCTTTCGANA 121

RESULT 10
 AZ926128/c
 LOCUS 454 bp DNA linear GSS 01-APR-2001
 DEFINITION 476.dio41e06.sl Saccharomyces castellii NRRL Y-12630 Saccharomycetes
 castellii genomic clone 476.dio41e06.sl, genomic survey sequence.
 AZ926128
 AZ926128.1 GI:13497029
 GSS.
 Saccharomyces castellii
 Saccharomycetes castellii
 Saccharomycetes
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 1 (bases 1 to 454)
 Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T.,
 Gish, W.R., Waterston, R.H. and Johnston, M.
 Surveying Saccharomycetes genomes to identify functional elements by
 comparative DNA sequence analysis
 Unpublished (2001)
 Contact: Johnston M
 Department of Genetics
 Washington University Medical School
 Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
 Tel: 314 362 2735
 Fax: 314 362 7855
 Email: mj@genetics.wustl.edu
 Class: random plasmid subclone.
 Location/Qualifiers

FEATURES

source
 1..454
 /organism="Saccharomyces castellii"
 /mol_type="genomic DNA"
 /strain="NRRL Y-12630 (CBS 4309)"
 /db_xref="taxon:27288"
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 /clone_lib="Saccharomyces castellii NRRL Y-12630"
 /note="Random genomic sequence"

FEATURES

source
 1..454
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 /db_xref="taxon:27288"
 /clone="476.dio41e06.sl"
 /clone_lib="Saccharomyces castellii NRRL Y-12630"
 /note="Random genomic sequence"

FEATURES

source
 1..454
 /organism="Saccharomyces castellii"
 /mol_type="genomic DNA"
 /strain="NRRL Y-12630 (CBS 4309)"
 /db_xref="taxon:27288"
 /clone="476.dio41e06.sl"
 /clone_lib="Saccharomyces castellii NRRL Y-12630"
 /note="Random genomic sequence"

ORIGIN

Query Match 21.0%; Score 90.6; DB 11; Length 454;
 Best Local Similarity 66.8%; Pred. No. 8.9e-14;
 Matches 129; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 239 CCAAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATCGCTCAGAGATTCAAGACGCTT 298
 DB 454 CAAAGCCCTTAGTGTGTTGCAATTGAATGAATGATGATGGTCTGCTGAATCCCAAGCCT 395

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Qy 299 TAGAAGAAATCTCGGCGCAAAAAAAGTGTACTTAAGTATACATCAATGCGAAGCACATTG 358
Db 394 TATTTGAAATTAATGCGCAAAAGACCGTTCCAAATATTTACATCAATGGTAAGCACGTTG 335
Qy 359 GTGCTACAGCATTTGGAAACTTTTGAAGAAAATGCGAAGTTAGCTGAATATTGAAGC 418
Db 334 GTGGGAACGATTAATTCAGACTTGAAGAATCTGGTGAATTTGAAGATTTATTGGAGC 275
Qy 419 CGGTATTTCATA 431
Db 274 CAATCTGGAGTA 262

RESULT 11
LOCUS C2286838 848 bp DNA linear GSS 01-JUL-2005
DEFINITION cp49c01.r Candida parapsilosis Random Genomic Library Candida
parapsilosis genomic clone cp49c01, genomic survey sequence.
ACCESSION C2286838
VERSION C2286838
KEYWORDS GSS.
SOURCE Candida parapsilosis
ORGANISM Candida parapsilosis
REFERENCE 1 (bases 1 to 848)
AUTHORS Logue, M.E., Wong, S., Wolfe, K.H. and Butler, G.
TITLE A genome sequence survey shows that the pathogenic yeast Candida
parapsilosis has a defective MTUAI allele at its mating type locus
JOURNAL Eukaryot. Cell 4 (6), 1009-1017 (2005)
PUBMED 15947193
COMMENT Contact: Logue M
Department of Biochemistry, Conway Institute of Biomolecular and
Biomedical Research
University College Dublin
Dublin 4, Ireland
Tel: +353 1 7166885
Fax: +353 1 2837211
Email: mary.e.logue@ucd.ie
Class: plasmid ends.
FEATURES
Location/Qualifiers
1..848
/organism="Candida parapsilosis"
/mol_type="genomic DNA"
/strain="CLIB214"
/db_xref="taxon:5480"
/clones="cp49c01"
/clone_lib="Candida parapsilosis Random Genomic Library"
ORIGIN
Query Match 16.8%; Score 72.4; DB 13; Length 848;
Best Local Similarity 59.1%; Pred. No. le-08;
Matches 149; Conservative 0; Mismatches 91; Indels 12; Gaps 1;
Qy 150 AAAGGAAGTGTGTTGTCAGCAAGACATCTGCCCTTACTGTCTAGTAAAGCTATTGTCTAC 209
Db 444 AAACAAGATCTTACTGTATTCAAAAACCTACTGCCCTTATTGACCCGCCAACGATTT 385
Qy 210 CCTCTTCCAGAAATGTAACGTTCCCAATCCAAAGCCCTTGTGTGTAATAGATGAAT 269
Db 384 ACTAGGAAGATGTGGATCGATTACAAAT-----TGATTGAATGAATACAAC 337
Qy 270 GAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAATCTCGGCCCAAAAACCTGTACC 329
Db 336 TTCAGATGGCGGTGAGGTTTCAGCGTGCACTACAGAATAACAGCGGTCAAAAGAACTGTACC 277
Qy 330 TAACGTATACATCAATGCAAGCACATTTGGTGGTAAACAGCGATTGTGAAAACCTTTGAAGAA 389
Db 276 AAATGTTTTTCATCAATGGTGAGCATATCGGAGGTAATCTGATTTGCAAGCCTTAGAGAG 217
Qy 390 AAATGGCAAGTT 401
Db 216 TAAAGGAGAGTT 205

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RESULT 12

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LOCUS DN156309 492 bp mRNA linear EST 18-FEB-2005
DEFINITION GCA001D02x GCA Hordeum vulgare cDNA clone GCA001D02 3-PRIME, mRNA
sequence.
ACCESSION DN156309
VERSION DN156309.1 GI:59942203
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
REFERENCE 1 (bases 1 to 492)
AUTHORS Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,
Schaefer, W., Schoiz, U., Sonnwald, U., Sonnwald, U. and Kogel, K.H.
TITLE Barley ESTs from different tissues challenged with fungal pathogens
JOURNAL Unpublished (2004)
COMMENT Contact: Sophia Biemelt
Molecular Developmental Physiology, Department Molecular Cell
Biology
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466 Gatersleben, Germany
Tel: +49 (0) 39482-5476
Fax: +49 (0) 39482-5515
Email: biemelt@ipk-gatersleben.de
Insert length: 492 Std Error: 0.00
Plate: 1 row; D column: 2
Seq primer: pTriplex2.
FEATURES
Location/Qualifiers
1..492
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Chevron"
/db_xref="GABI:1083101"
/db_xref="taxon:4513"
/clone="GCA001D02"
/tissue_type="with Fusarium graminearum infected
spikelets"
/lab_host="E. coli BM25.8"
/clone_lib="GCA"
/notes="Vector: pTriplex2 (BD Biosciences); Site 1: SfIA
(GGCCATTATGGCC); Site 2: SfIB (GGCCGCTCGGCC); Each second
spikelet of barley was infected with Fusarium graminearum
(strain FG2311, isolated from wheat, 1992, Hohenheim,
Germany) by means of micropipette using 5 microliter of
conidia suspension (500 conidia /microliter). The infected
plants were incubated 4d by 16 h light and 20 degree
celcius and infected spikes were incubated the first 48 h
by 100 % rel. humidity for establishing of infection.
PolyA-RNA was isolated from infected spikes and used to
create a cDNA-library using the Creator Lambda Triplex2
libraries kit (BD Biosciences). cDNA Fragments were
inserted into the vector pLambda-Triplex2. Subsequently,
plasmids were obtained by in vivo excision according to
manufacturers instruction. (GABI-Agrotech project)"
ORIGIN
Query Match 15.9%; Score 68.8; DB 9; Length 492;
Best Local Similarity 54.6%; Pred. No. 9e-08;
Matches 167; Conservative 0; Mismatches 127; Indels 12; Gaps 1;
Qy 116 AAACAGTGTCTACGTAAGGATCTGATTGGCCAAAGGAAGTGTGTTGGCGAAGAAGA 175
Db 32 AAGCATCTACCAAGGTTTCAGACGTTATCGACAACAACCTCTGTTGTCTCTCCAAAGT 91
Qy 176 CATCTGCCCTTACTGTAAGCTACTTTGTCTACCTCTTCCAGAAATGAAGCTTCCCA 235
Db 92 CTTACTGCCCTTACTGCAAGACGACCAAGAAGATC-----TGGATGATTGA 139
Qy 236 AATCCAAGGCCCTTGTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACG 295

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Qy      356  TTGGTGGTACACGCGATTTCGAACTTTGAAGAAATATGCAAGTTAGCTGAATATTGA 415
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Db      320  AGGAGG 325

RESULT 13
CN813116/c
LOCUS      CN813116      529 bp      mRNA      linear      EST 01-JUN-2004
DEFINITION Fg06_03g17_R Fg06_AAF_C_ECORC_Fusarium_graminearum_perithecia
CN813116
VERSION     CN813116.1 GI:47837127
KEYWORDS
SOURCE      Gibberella zeae (anamorph: Fusarium graminearum)
ORGANISM    Gibberella zeae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE   1 (bases 1 to 529)
AUTHORS     Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J.,
            Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M.,
            Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
TITLE       Expressed Sequence Tags from Fusarium graminearum enriched for late
            stage perithecia
JOURNAL     Unpublished (2004)
COMMENT     Contact: Harris, Linda J.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
            CANADA
            Tel: (613) 759-1314
            Fax: (613) 759-6566
            Email: harrislj@agr.gc.ca.

FEATURES             source
     1..529
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         /mol_type="mRNA"
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         /note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown
         on carrot agar at 200C until confluent; perithecia induced
         with Tween 40 solution (25% v/v). Fruiting bodies were
         collected 20 days after induction. Total RNA was extracted
         using Trizol. cDNAs were amplified using Invitrogen
         GeneRacer kit. cDNA was not fractionated and was
         bidirectionally cloned."

ORIGIN
Query Match      15.8%; Score 68.4; DB 8; Length 529;
Best Local Similarity 54.2%; Pred. No. 1.2e-07;
Matches 166; Conservative 1; Mismatches 127; Indels 12; Gaps 1;

Qy      116  AACAGTTGCTCAGTAAGGATCTGATGGCCAAAAGGAAGTGTGTTGTCAGCAAGA 175
Db      491  AAGCATCTACCAAGGTTACAGCAGCTTATCGACAACAACCTCTGTTGTTGTTCTTCCAAGT 432
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Db      383  ACACCGAGTACGAGCTCTTGGCTCGACGAAGTTTCCGATGCTGCTCTCCAGGACG 324
Qy      296  CTTTAGAAGAAATCTCGGCGCAAAAATCTGACTACCTATACATCAATGCGAAGCACA 355
Db      323  CTCTCGAAGAAGATSTCTGGCCAGCGTACCGTCCCAACGCTTACATCAAGCAGCAGCACA 264
Qy      356  TTGGTGGTAACTGGAATTTGGAAATTTGAAGAAATATGCAAGTTAGCTGAATATTGA 415
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Qy      416  AGCCGG 421
Db      203  AGGAGG 198

RESULT 14
CN813786
LOCUS      CN813786      522 bp      mRNA      linear      EST 01-JUN-2004
DEFINITION Fg06_04h05_R Fg06_AAF_C_ECORC_Fusarium_graminearum_perithecia
CN813786
VERSION     CN813786.1 GI:47837797
KEYWORDS
SOURCE      Gibberella zeae (anamorph: Fusarium graminearum)
ORGANISM    Gibberella zeae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE   1 (bases 1 to 522)
AUTHORS     Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J.,
            Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M.,
            Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
TITLE       Expressed Sequence Tags from Fusarium graminearum enriched for late
            stage perithecia
JOURNAL     Unpublished (2004)
COMMENT     Contact: Harris, Linda J.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
            CANADA
            Tel: (613) 759-1314
            Fax: (613) 759-6566
            Email: harrislj@agr.gc.ca.

FEATURES             source
     1..522
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         /note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown
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         with Tween 40 solution (25% v/v). Fruiting bodies were
         collected 20 days after induction. Total RNA was extracted
         using Trizol. cDNAs were amplified using Invitrogen
         GeneRacer kit. cDNA was not fractionated and was
         bidirectionally cloned."

ORIGIN
Query Match      15.7%; Score 68; DB 8; Length 522;
Best Local Similarity 52.9%; Pred. No. 1.5e-07;
Matches 162; Conservative 6; Mismatches 126; Indels 12; Gaps 1;

Qy      116  AACAGTTGCTCAGCTAAGGATCTGATGGCCAAAAGGAAGTGTGTTGTCAGCAAGA 175
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Db 320 AGGAGG 325
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RESULT 15
CD459632/c
LOCUS
DEFINITION
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  Fg09_06j07 A Fg09 AAFc ECORC Fusarium graminearum simple_substrate
  Gibberella zeae cDNA clone Fg09_06j07, mRNA sequence.
VERSION
  CD459632.2 GI:48689774
KEYWORDS
  EST.
ORGANISM
  Gibberella zeae (anamorph: Fusarium graminearum)
  Gibberella zeae
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
  1 (bases 1 to 477)
  Watson, R.J., Heys, R., Couroux, P., De Moors, A., Harris, L.J.,
  Hattori, J., Lacroix, C., Masotti, M., Ouellet, T., Robert, L.S.,
  Singh, J.A., Sprott, D. and Tinker, N.A.
  A cDNA library prepared from Fusarium graminearum grown on a simple
  substrate
  Unpublished (2003)
  On Jun 3, 2003 this sequence version replaced gi:31374372.
  Contact: Watson, Robert.J.
  Eastern Cereal and Oilseed Research Centre
  Agriculture and Agri-food Canada
  Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
  CANADA
  Tel: (613) 759-1655
  Fax: (613) 759-1701
  Email: watsonrj@agr.gc.ca.
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      /note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
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ORIGIN

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Query Match 15.6%; Score 67.6; DB 5; Length 477;
Best Local Similarity 55.2%; Pred. No. 1.9e-07;
Matches 158; Conservative 1; Mismatches 115; Indels 12; Gaps 1;
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QY 176 CATACTGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAAGAATTGAACGTTCCCA 235
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Db 388 CTTACTGCCCTTACTGCAAGCAGACCAAGAGACTC-----TGGATGATTGA 341
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|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 340 ACACCCAGTAGCAGACTCTTTGAGCTCGACGAAGTTTCCGATGCTCTGCTCTCCAGGACG 281
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Db 220 TTGGTGTAACTCAGACCTCCAGACCTGAACTCTGGCGAAAGCTCAAGAMCTTCTCA 175
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Job time : 4444 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Title: US-10-523-362-3

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Searched: 1403666 seqs, 93554401 residues

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Listing first 45 summaries

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- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	75.2	17.4	183	3	US-09-248-796A-4011 Sequence 4011, Ap
2	69.8	16.2	582	3	US-09-248-796A-4012 Sequence 4012, Ap
3	64.6	15.0	681	3	US-08-998-416-1146 Sequence 1146, Ap
4	45.6	10.6	453	3	US-09-270-767-758 Sequence 758, App
5	45.6	10.6	453	3	US-09-270-767-16040 Sequence 16040, A
6	44	10.2	302	3	US-09-313-294A-4085 Sequence 4085, Ap
7	43.2	10.0	497	3	US-09-621-976-1270 Sequence 1270, Ap
8	43.2	10.0	654	2	US-08-911-319A-2 Sequence 2, Appli
9	43.2	10.0	654	3	US-09-352-619-2 Sequence 2, Appli
10	42	9.7	2191	3	US-09-127-219B-1 Sequence 1, Appli
11	39	9.0	522	3	US-09-162-564-1 Sequence 1, Appli
12	38.8	9.0	474	3	US-09-621-976-1272 Sequence 1272, Ap
13	37.4	8.7	519	3	US-09-513-999C-3976 Sequence 3976, Ap
14	36.4	8.4	530	3	US-09-621-976-1271 Sequence 1271, Ap
15	36.2	8.4	837	4	US-09-880-107-3793 Sequence 3793, Ap
16	34.8	8.1	580073	3	US-08-545-528B-1 Sequence 1, Appli
17	34.6	8.0	1830121	3	US-09-557-884-1 Sequence 1, Appli
18	34.6	8.0	1830121	3	US-09-643-990A-1 Sequence 1, Appli
19	34.6	8.0	1830121	3	US-10-158-865-1 Sequence 1, Appli
20	34.4	8.0	603	3	US-09-533-559-3294 Sequence 3294, Ap
21	34.4	8.0	3258	3	US-09-328-352-587 Sequence 587, App
22	34.4	8.0	9408	3	US-09-418-710-14 Sequence 14, Appl
23,	34.4	8.0	9408	3	US-09-839-479-14 Sequence 14, Appl

24	34.2	7.9	479	3	US-08-899-786-17	Sequence 17, Appl
25	34.2	7.9	1103	3	US-08-899-786-13	Sequence 13, Appl
26	34	7.9	77586	3	US-09-949-016-13220	Sequence 13220, A
27	34	7.9	77586	3	US-09-949-016-13221	Sequence 13221, A
C 28	33.6	7.8	474	3	US-09-621-976-18033	Sequence 18033, A
C 29	33.6	7.8	601	3	US-09-949-016-132474	Sequence 132474, A
C 30	33.6	7.8	601	3	US-09-949-016-173301	Sequence 173301, A
C 31	33.6	7.8	601	3	US-09-949-016-173302	Sequence 173302, A
C 32	33.6	7.8	141248	3	US-09-949-016-12241	Sequence 12241, A
C 33	33.6	7.8	143248	3	US-09-949-016-16652	Sequence 16652, A
C 34	33.6	7.8	450395	3	US-09-949-016-15473	Sequence 15473, A
C 35	33.6	7.8	451924	3	US-09-949-016-12896	Sequence 12896, A
C 36	33.6	7.8	451925	3	US-09-949-016-17305	Sequence 17305, A
C 37	33.6	7.8	636591	3	US-09-949-016-11808	Sequence 11808, A
C 38	33.6	7.8	636591	3	US-09-949-016-13388	Sequence 13388, A
C 39	33.2	7.7	468	3	US-09-134-000C-1668	Sequence 1668, Ap
40	33.2	7.7	484	3	US-08-899-786-18	Sequence 18, Appl
41	33.2	7.7	549	3	US-09-328-352-3243	Sequence 3243, Ap
C 42	33.2	7.7	601	3	US-09-949-002-7829	Sequence 7829, Ap
C 43	33.2	7.7	267482	3	US-09-949-002-659	Sequence 659, App
C 44	33.2	7.7	267505	3	US-09-949-002-783	Sequence 783, App
45	33	7.6	291	3	US-09-543-681A-1044	Sequence 1044, Ap

ALIGNMENTS

RESULT 1

US-09-248-796A-4011
; Sequence 4011, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 4011

; LENGTH: 183

; TYPE: DNA

; ORGANISM: Candida albicans

US-09-248-796A-4011

Query Match	17.4%	Score 75.2;	DB 3;	Length 183;
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Matches 110;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;
QY	254	TGGAATTAGATGAAATGACCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGG	313	
Db	11	TTGAATTAGCAAGAGTTGACGCGGTGTAATCCAGAGCATTTATTGGAATCACTG	70	
QY	314	GCACAAACTGTACTTACCTATACATCAATGGCAGCACATTCGTTGGAACAGGATT	373	
Db	71	GTCAAGAACCGTTCCTCAATGCTTTATTGGTGGTCAACATATTGGTGGCAATTCGATG	130	
QY	374	TGCAAACTTTGAAGAAATGCAAGTTAGCTGAAATATTGAAGCCGG	421	
Db	131	TGCAGCTTTGAATCTTATGACATTTAATAACAATTCAACTG	178	

RESULT 2

US-09-248-796A-4012

; Sequence 4012, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

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; ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; ; FILE REFERENCE: 107196.132
; ; CURRENT APPLICATION NUMBER: US/09/248,796A
; ; CURRENT FILING DATE: 1999-02-12
; ; PRIOR APPLICATION NUMBER: US 60/074,725
; ; PRIOR FILING DATE: 1998-02-13
; ; PRIOR APPLICATION NUMBER: US 60/096,409
; ; PRIOR FILING DATE: 1998-08-13
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; ; ORGANISM: Candida albicans
US-09-248-796A-4012

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RESULT 3
US-08-998-416-1146
; Sequence 1146, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgin
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; NUMBER OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET INFORMATION: PF/5-30306/A/GCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689

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; INFORMATION FOR SEQ ID NO: 1146:
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 681 base pairs
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;     STRANDEDNESS: single
;     TOPOLOGY: linear
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; MOLSECU TYPE: DNA (genomic)
;
; ORIGINAL SOURCE:
;
; ORGANISM: PAG1696UP
;
; US-08-998-416-1146

```

Query Match	15.0%;	Score 64.6;	DB 3;	Length 681;
Best Local Similarity	55.0%;	Pred. No. 1.5e-09;		
Matches 149;	Conservative 0;	Mismatches 119;	Indels 3;	Gaps 1;
QY	100	AAATGGTATCCAGGAAACAGTTGCTCAGGTAAGGATCTGATGGCCAAAGGAAGTG	159	
DB	410	ATAATGGTTTCCCTTTCCGTTATTAAACAGGTGCAGCGCTAATCCAGCAGAACCCGCGTG	469	
QY	160	TTTGTTTGCAGCAAGACATACTCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAA	219	
DB	470	TTCAATTGCATCCAAAGACGTACTGTCCGTATTGCAGCGCCAAAGCGTACTGCTCGAG	529	
QY	220	GAAATTGAACGTTCCCAAAATCCAAAGGCCCTTGTGTTGGAAATTAGATGAAATGAGCAAT---	276	
DB	530	GAGAAGCGGTCCCGCAAGCGCAGTAAAACTCTTGGAGCTTGACACCATGGCGGAGGAG	589	
QY	277	GGCTCAGAGATTCAGACGCTTTAGAGAATAATCTCGGGCCAAAAAATCTGTACCTAAGCTA	336	
DB	590	GGCGCGGTATCCAAAGCGCGTTGCAGGAGCTGAGCGGGCAGCGCAGCGTGCACCAATC	649	
QY	337	TACATCAATGGCAAGCACATTGGTGGTTACA	367	
DB	650	TACATCAACGGCGCCCATGTGGGTGCAACA	680	

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RESULT 4
US-09-270-767-758
; Sequence 758, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 758
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-758

```

	Query Match	10.6%	Score 45.6	DB 3	Length 453
	Best Local Similarity	54.9%	Pred. No. 0.00072		
	Matches	90	Conservative	0	Mismatches 74
				Indels	Gaps
				0	0
Qy	234	CAAAATCAAGGCCCTTGTGTGCAATTTAGATGAAATGAGCAATGGCTCAGAGATTCAAGA	293		
Db	256	CAACGTCAAGGCCAACGGTGATTCAGCTGGACACGGGATGTGGCAACAGAGATCCAGGC	315		
Qy	294	CGCTTTTAGAAGAAATCTCGGGCCAAAAAAGTGTACCTTACGTATACATCATATGCGCAAGCA	353		
Db	316	GGTTCCTGGCGAGATGACGGGCTCGAGGACCGTTCACAGTTGCTTCATCGATGSCAAATT	375		
Qy	354	CATTGGTGTAAACAGCGATTTGGAAACTTTGGAAGAAAAATGGCA	397		
Db	376	CGTGGGTGGCGGCACCGACGTGAAGCGGCTATACGAACAGGGCA	419		

RESULT 5
US-09-270-767-16040

; Sequence 16040, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16040
; LENGTH: 453
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-16040

Query Match 10.6%; Score 45.6; DB 3; Length 453;
Best Local Similarity 54.9%; Pred. No. 0.00072;
Matches 90; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 234 CAAATCCAAGGCCCTTGTTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGA 293
DB 256 CAAGCTCAGGCAACGGTGATCGAGCTGGACCAGCGGATGATGGCAACGAGATCCAGGC 315
QY 294 CGCTTTAGAGAAATCTCGGCCAAAACCTGTACCTAATCATATACATCAATGCGCAAGCA 353
DB 316 GGTCTTTGGGAGATGACGGCTCGAGACCGTTCCACGTTGCTTCATCGATGCGCAAGTT 375
QY 354 CATTGGTGTACAGCATTTGGAACTTTGAAGAAAATGGCA 397
DB 376 CGTGGTGGCGGCCACCGAGCTGAAGCGGCTATACGACAGGGCA 419

RESULT 6

US-09-313-294A-4085
; Sequence 4085, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4085
; LENGTH: 302
; TYPE: DNA
; ORGANISM: *Zea mays*
; FEATURES:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6476212 700347664H1
; NAME/KEY: unsure
; LOCATION: 2, 27, 106, 120, 130, 162, 189, 287
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4085

Query Match 10.2%; Score 44; DB 3; Length 302;
Best Local Similarity 62.4%; Pred. No. 0.0018;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 254 TGAATTAGAATGAGCAATGGCTCAGAGATTCAGAGCTTTAGAGAAATCTCGG 313
DB 174 TTGAGTTGGATGAGNCAGTGTGAGCTGAGCTCCAGAAATGCCCTGAAGAGTGGACTG 233
QY 314 GCCAAAACCTGTACCTAATCATATACATCAATGCGCAAGCACATTGGTGG 362
DB 234 GACAGAGACTGTCCCAAAATGCTTCATCAATGGAAGACATATTGGCGG 282

RESULT 7

US-09-621-976-1270
; Sequence 1270, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1270
; LENGTH: 497
; TYPE: DNA
; ORGANISM: *Homo sapiens*
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 154..495
US-09-621-976-1270

Query Match 10.0%; Score 43.2; DB 3; Length 497;
Best Local Similarity 55.3%; Pred. No. 0.004;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 250 GTGTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAGAGACGCTTTAGAGAAATC 309
DB 319 GTGTGGAACTGGACCTGCTTGAATATGAAACAGGTTCAGAGATGCTCTTTACAAATG 378
QY 310 TCGGGCCAAAACCTGTACCTAATCATATACATCAATGGCAAGCACATTTGGTGGTAAACGC 369
DB 379 ACTGGTGAAGAACTGTTCAGAAATATTTGTCAATGCTATTTTATTGGAGGTGCAACT 438
QY 370 GATTGGAACTTTGAAGAAAATGCGCAAGTT 401
DB 439 GACACTCATAGGCTTCACAAAGGAAGAAAT 470

RESULT 8

US-08-911-319A-2
; Sequence 2, Application US/08911319A
; Patent No. 5968798
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,319A
; FILING DATE: August 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555

```
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829
US-08-911-319A-2

Query Match          10.0%; Score 43.2; DB 2; Length 654;
Best Local Similarity 55.3%; Pred. No. 0.0045;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 250 GTGTTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATC 309
DB 296 GTGGTGGAACTGGACCTGCTGAATATGGAACCAAGTTCGAAGATGCTTTTACAAAATG 355
QY 310 TCGGGCCAAAACCTGTACCTAACGTATACATCAATGCGCAAGCACATTGGTGGTACAGC 369
DB 356 ACTGGTGAAGAACTGTTCGAAGAATATTGTCAATGGTACTTTTATTGGAGGTGCAACT 415
QY 370 GATTGGAACTTTGAGAAAAAATGCGAAGTT 401
DB 416 GACACTCATAGGCTTCACAAAGAGGAAAAAT 447

RESULT 9
US-09-352-619-2
; Sequence 2, Application US/09352619
; Patent No. 6084070
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,619
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,319
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Muenzen, Colette C.
; REGISTRATION NUMBER: 39,784
; REFERENCE/DOCKET NUMBER: PF-0363 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829

; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPINOT03
; CLONE: 2447829

US-09-352-619-2
; Sequence 1, Application US/09127219B
; Patent No. 6372772
; GENERAL INFORMATION:
; APPLICANT: KIRKPATRICK, D. LYNN
; APPLICANT: POWIS, GARTH
; TITLE OF INVENTION: INHIBITORS OF REDOX SIGNALING AND METHODS OF USING SAME
; FILE REFERENCE: 98-571-us
; CURRENT APPLICATION NUMBER: US/09/127,219B
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/054,566
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-127-219B-1

Query Match          9.7%; Score 42; DB 3; Length 2191;
Best Local Similarity 60.5%; Pred. No. 0.017;
Matches 69; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 249 TGTGTTGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAAT 308
DB 94 TGTCTTGGAACTTGATCAAGTTGATGGGGCCAGGGTTCAAGAAAGTGCTGTCTCAGAAAT 153
QY 309 CTCGGGCCAAAACCTGTACCTAACGTATACATCAATGCGCAAGCACATTGGTGG 362
DB 154 CACTAATCAGAAAACTGTGCCCAATATTTCGTGAATAAAGTCATGTAGGTGG 207

RESULT 11
US-09-162-564-1
; Sequence 1, Application US/09162564
; Patent No. 6379664
; GENERAL INFORMATION:
; APPLICANT: Lou, Marjorie
; APPLICANT: Raghavachari, Nalini
; APPLICANT: Qiao, Fengyu
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR THE PREVENTION AND TREATMENT
; FILE REFERENCE: UNL-98-2-1
; CURRENT APPLICATION NUMBER: US/09/162,564
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (4)...(324)
US-09-162-564-1

Query Match      9.0%; Score 39; DB 3; Length 522;
Best Local Similarity 58.0%; Pred. No. 0.076;
Matches 69; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 283 GAGATTCACAGACGCTTTAGAGAAATCTCGGGCCAAAATACTGTACCTAACGTTATACATC 342
Db 169 GAGATTCACAGATTTATCTGCAACAGCTCACAGGACCCAGACGGTACCTCGGTCCTTTATC 228

Qy 343 AATGGCAAGCACATTTGGTGTAAACAGGATTTGAAACTTTGAAGAAAATGGCAAGTT 401
Db 229 GGTAAGAGTGTATAGTGGATGCTGATCTAGAAAGTATGCAACAGAGAGGGGAGCT 287

RESULT 12
US-09-621-976-1272
; Sequence 1272, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1272
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 193..474
US-09-621-976-1272

Query Match      9.0%; Score 38.8; DB 3; Length 474;
Best Local Similarity 58.8%; Pred. No. 0.083;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 250 GTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAATC 309
Db 358 GTGTTGGAATGGACCTGCTTGAATATGGAACCAAGTCCAAAGATGCTCTTTACAAATG 417

Qy 310 TCGGGCCAAAATACTGTACCTAACGTATACATCAATGGCAAGCACATTTGGTGGT 363
Db 418 ACTGTGAAGAACTGTTCCAAGATATTTGTCAATGCTACTTTTATTTGGAGGT 471

RESULT 13
US-09-513-999C-3976
; Sequence 3976, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3976
; LENGTH: 519
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..433
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 340
; OTHER INFORMATION: y=c or t
US-09-513-999C-3976

Query Match      8.7%; Score 37.4; DB 3; Length 519;
Best Local Similarity 57.5%; Pred. No. 0.23;
Matches 65; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

Qy 283 GAGATTCACAGACGCTTTAGAGAAATCTCGGGCCAAAATACTGTACCTAACGTTATACATC 342
Db 281 GAGATTCACAGATTTATTTGCAACAGCTCACGGGAGCAAGACGGTGCCTCGAGTCTTATY 340

Qy 343 AATGGCAAGCACATTTGGTGTAAACAGGATTTGGAACCTTTGAAGAAAATGG 395
Db 341 GGTAAAGATTTGATAGCGGATGCGAGTATAGTCTCTTTGCAACAGAGTGG 393

RESULT 14
US-09-621-976-1271
; Sequence 1271, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1271
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 378..530
US-09-621-976-1271

Query Match      8.4%; Score 36.4; DB 3; Length 530;
Best Local Similarity 58.2%; Pred. No. 0.46;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 250 GTGTTGGAATTAGATGAATGAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAATC 309
Db 420 GTGTTGGAATGGACCTGCTTGAATATGGAACCAAGTTCCAAGATGCTCTTTACAAATG 479

Qy 310 TCGGGCCAAAATACTGTACCTAACGTATACATCAATGGCAAGCACATTTGG 359
Db 480 ACTGTGAAGAACTGTTCCAAGATATTTGTCAATGGTACTTTTATTGG 529

RESULT 15
US-09-880-107-3793
; Sequence 3793, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:35:08 ; Search time 1459 Seconds
(without alignments)
3638.285 Million cell updates/sec

Title: US-10-523-362-3

Perfect score: 432

Sequence: 1 atggagacaaattttccctt.....tgaagccggtatttcaatag 432

Scoring table: IDENTITY NUC

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Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SID33/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SID33/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SID33/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SID33/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SID33/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SID33/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SID33/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SID33/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SID33/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432	100.0	432	11	US-10-932-182A-76174
2	432	100.0	432	12	US-10-523-362-3
3	432	100.0	932	8	US-10-451-467A-133
4	336.6	77.9	570	11	US-10-932-182A-3898
5	153.8	35.6	345	11	US-10-932-182A-3588
6	147.4	34.1	833	8	US-10-451-467A-65
7	146.6	33.9	333	11	US-10-932-182A-75707
8	143.4	33.2	333	12	US-10-523-362-1
9	89	20.6	360	7	US-10-032-585-6780
10	89	20.6	360	8	US-10-451-467A-607
11	61	14.1	609	9	US-10-425-115-146552
12	56	13.0	377	9	US-10-425-115-149360
13	56	13.0	578	16	US-11-096-568A-26783
14	55.6	12.9	721	8	US-10-437-963-29343
15	55.6	12.9	733	12	US-10-523-362-47
16	55	12.7	278	3	US-09-923-876-5514
17	55	12.7	278	3	US-09-923-876-5514

18	55	12.7	628	12	US-10-523-362-45	Sequence 45, Appl
19	55	12.7	763	9	US-10-425-115-44746	Sequence 44746, A
20	55	12.7	788	8	US-10-437-963-47111	Sequence 47111, A
21	55	12.7	877	9	US-10-425-115-44748	Sequence 44748, A
22	54.8	12.7	336	12	US-10-523-362-25	Sequence 25, Appl
23	53.2	12.3	649	9	US-10-425-115-177299	Sequence 177299, A
24	53.2	12.3	657	12	US-10-523-362-15	Sequence 15, Appl
25	50.2	11.6	628	8	US-10-767-701-11104	Sequence 11104, A
26	50	11.6	540	12	US-10-523-362-33	Sequence 33, Appl
27	49.2	11.4	449	3	US-09-535-459-73	Sequence 73, Appl
28	49.2	11.4	596	8	US-10-767-701-11645	Sequence 11645, A
29	49.2	11.4	597	9	US-10-425-115-127828	Sequence 127828, A
30	49.2	11.4	621	8	US-10-425-114-16796	Sequence 16796, A
31	49.2	11.4	864	8	US-10-425-114-25338	Sequence 25338, A
32	49.2	11.4	1579	9	US-10-425-115-127829	Sequence 127829, A
33	47.2	10.9	779	8	US-10-437-963-52359	Sequence 52359, A
C	34	47	282	11	US-10-932-182A-79774	Sequence 79774, A
35	46.8	10.8	385	3	US-09-732-627A-1485	Sequence 1485, Ap
36	46.8	10.8	590	8	US-10-021-323-8409	Sequence 8409, Ap
37	46.4	10.7	529	3	US-09-732-627A-628	Sequence 628, App
38	46.2	10.7	463	8	US-10-767-701-20293	Sequence 20293, A
39	46	10.6	481	9	US-10-425-115-123588	Sequence 123588, A
40	45.6	10.6	446	13	US-11-097-143-17639	Sequence 17639, A
41	45.6	10.6	478	13	US-11-097-143-15011	Sequence 15011, A
42	45.6	10.6	805	9	US-10-425-115-62369	Sequence 62369, A
43	45.6	10.6	1590	9	US-10-425-115-62371	Sequence 62371, A
44	45.6	10.6	2446	13	US-11-097-143-17638	Sequence 17638, A
45	45.4	10.5	672	12	US-10-523-362-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-932-182A-76174

; Sequence 76174, Application US/10932182A

; Publication No. US20060046253A1

; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: 030685-043

; CURRENT APPLICATION NUMBER: US/10/932,182A

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 76174

; LENGTH: 432

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-10-932-182A-76174

Query Match 100.0%; Score 432; DB 11; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGAGACCAATTTTCTTCGACTCGAATTTAATTTGTTTATTATCAATATCAGCTGTTT	60
Db	1	ATGGAGACCAATTTTCTTCGACTCGAATTTAATTTGTTTATTATCAATATCAGCTGTTT	60
Qy	61	GCACAGAATTTTCTTAAGATTTTATCTACTCCAAATGTTTCCAGGAAACA	120
Db	61	GCACAGAATTTTCTTAAGATTTTATCTACTCCAAATGTTTCCAGGAAACA	120
Qy	121	GTGCTCAGCTAAAGATCTGATTGCGCAAGAGAGTGTGTTGTCAGCAAGACATAC	180
Db	121	GTGCTCAGCTAAAGATCTGATTGCGCAAGAGAGTGTGTTGTCAGCAAGACATAC	180
Qy	181	TGCCCTTACTGTAAGCTACTTTTGTCTACCCCTTCCAAAGAAATGACGTTCCCAATCC	240

Db 181 TGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Qy 241 AAGGCCCTTGTGTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 241 AAGGCCCTTGTGTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Qy 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Qy 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Db 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432
RESULT 2
US-10-523-362-3
; Sequence 3, Application US/10523362
; Publication No. US20060064784A1
; GENERAL INFORMATION:
; APPLICANT: Chardomans, Agnes
; APPLICANT: Puzio, Piotr
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: 532622010300
; CURRENT APPLICATION NUMBER: US/10/523,362
; CURRENT FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
; OTHER INFORMATION:
US-10-523-362-3
Query Match 100.0%; Score 432; DB 12; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTTATCATTTACGTTGTTT 60
Db 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTTATCATTTACGTTGTTT 60
Qy 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 120
Db 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 120
Qy 121 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Qy 181 TGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Db 181 TGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Qy 241 AAGGCCCTTGTGTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 241 AAGGCCCTTGTGTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Qy 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Qy 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420

Db 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Qy 421 GTATTTCAATAG 432
Db 421 GTATTTCAATAG 432
RESULT 3
US-10-451-467A-133
; Sequence 133, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REERKANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-133
Query Match 100.0%; Score 432; DB 8; Length 932;
Best Local Similarity 100.0%; Pred. No. 1.8e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTTATCATTTACGTTGTTT 60
Db 501 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATTTGTTATTTATCATTTACGTTGTTT 560
Qy 61 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 120
Db 561 GCCACAAGAAATTTATGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 620
Qy 121 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 180
Db 621 GTTGCTCAGCTAAAGGATCTGATTGGCCAAAAGGAAGTGTGTTGTCAGCAAGACATAC 680
Qy 181 TGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 240
Db 681 TGCCCTTACTGTAAAGCTACTTTGTCTACCCCTCTTCCAGAATTGAACGTTCCCAATCC 740
Qy 241 AAGGCCCTTGTGTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 741 AAGGCCCTTGTGTGGAATTAGATGAATAAGCAATGGCTCAGAGATTCAAGACGCTTTA 800
Qy 301 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 360
Db 801 GAAGAAATCTCGGCCCAAAAACGTGTACCTAAAGTATACATCAATGGCAGCACATTGGT 860
Qy 361 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Db 861 GGTAAACAGCATTTGGAAACTTTGAAGAAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 920
Qy 421 GTATTTCAATAG 432
Db 921 GTATTTCAATAG 932
RESULT 4

US-10-932-182A-3898

Sequence 3898, Application US/10932182A
Publication No. US20060046253A1
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHITHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3898
LENGTH: 570
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3898

Query Match 77.9%; Score 336.6; DB 11; Length 570;
Best Local Similarity 86.3%; Pred. No. 1.5e-84;
Matches 372; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGGAGACCAATTTTTCCTTCGACTCGAATTTAATTTATTTATTCATTATCACGTTGTTT 60
DB 139 ATGGAACCTAAATTTTCTTTTCGACTCAAAATTAATCGTTATTTGTCATTATCACGTTGTTT 198
QY 61 GCCACAGAATTTATGCTTAAGATTTTATCTACTCCAAAATGGTATCCAGGAACA 120
DB 199 GCCACAGAATTTATCGCTAAAGATTTTATCTACCCCAAAAATGGTATCTCAAGAAACA 258
QY 121 GTTGCTCAGTAAGATCTGATTCGCAAGGAAGTGTGTTGTCAGCAAGACATAC 180
DB 259 ATGCACAGTAAGACTTGATTCGCCAAGAGGTCCTCGTTGCGCGAAGACATAC 318
QY 181 TGCCCTTACTGTAAGACTACTTTGTCTACCCCTTTCCAGGAATTTGAAGTTCCCAATCC 240
DB 319 TGTGCTTACTGTAAGCCACATTTGTCACCTTTGTTCCAGGAATTTGAAGTTCTTAAATCC 378
QY 241 AGGCCCTTGTGTTGAATTAGAATGAGCAATGCTCAGAGATTCAGAGCGTTTA 300
DB 379 AAAGCGCTGTTGTTGAGTTGACGAAATGAGCAATGTTCCAGAAATCCAGGATGCTCTC 438
QY 301 GAAGAACTCGGGCCAAAACACTGCTACGATACATCAATGCAAGCAACATTTGTT 360
DB 439 GAAGAAATTTCCGGCCAAAGAACTGTACCAACGTTTACATCAATGTTAAGCAATCGGT 498
QY 361 GGTAAACAGGATTTGGAACACTTTGAAGAAAATGCGAAGTTAGCTGAAATTTGAAGCCG 420
DB 499 GGAACAGGATTTGGAAGCTTTGAAGAAAACGTAATTTGGCTGAATTTATTAAGACCG 558
QY 421 GTATTTCAATA 431
DB 559 GTTTTCGAATA 569

RESULT 5
US-10-932-182A-3588
Sequence 3588, Application US/10932182A
Publication No. US20060046253A1
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHITHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3588
LENGTH: 345
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3588

Query Match 35.6%; Score 153.8; DB 11; Length 345;
Best Local Similarity 67.1%; Pred. No. 7.3e-33;
Matches 218; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 95 CTCAAAAATGTTATCCAGGAAACAGTTGCTCAGTAAAGGATCTGATTGGCCAAAAGG 154
DB 5 CTAGAAATATGTTATCCCAAGAACTATCGATCAGCTCAGGAACTTTATTGCCGGAAGG 64
QY 155 AAGTGTGTTTGCAGCAAGACATATCTCCCTTACTGTAAAGCTACTTTGTCTACCCCTCT 214
DB 65 AAATTTGCTGCTCAGGAGCTACTGTCCATATCTGCCAGCGAGCGTTAAACACTCTGT 124
QY 215 TCCAAGATTTGAACGTTTCCCAATCCAAAGGCCCTTGTGTTTGAATTAGATGAATGACCA 274
DB 125 TCCAGAAATTTGAACGTTGCCAAAGTCCAAAGTCTCTGCTGCTGCAAGCGATGAAGG 184
QY 275 ATGGCTCAGAGATTTCAAGACGCTTTAGAGAAATCTCGGGCCAAAACACTGTACTCAACG 334
DB 185 AGGGCTGATATTCAGGAGCGCTTTGTACCAAGCTCAACGGCCAAAGAACCGTGCACAAACA 244
QY 335 TATACATCAATGGCAAGCACATTTGGTGTAAACAGCGATTTGGAAACTTTTGAAGAAAATG 394
DB 245 TCTACATCAACGTTAAGCATATTGGGGGGAACGACGACTTGCAGAGTTGCGTGAACCG 304
QY 395 GCAAGTTAGCTGAAATATTGAAGCC 419
DB 305 GCGAATTTGAAGAACTCTTGAAGCC 329

RESULT 6
US-10-451-467A-65
Sequence 65, Application US/10451467A
Publication No. US20040161840A1
GENERAL INFORMATION:
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMAN, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65
LENGTH: 833
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-65

Query Match 34.1%; Score 147.4; DB 8; Length 833;
Best Local Similarity 65.2%; Pred. No. 7.3e-31;
Matches 217; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 99 AAAAAATGTTATCCAGGAAACAGTTGCTCAGTAAAGATCTGATTGGCCAAAAGGAAAGT 158
DB 497 AAAAAATGTTATCTCAAGAACTATCAAGCAGCTCAAGGACCTTTATTCAGAAAACGAGAT 556
QY 159 GTTGTGTCAGCAAGACATATCGCTTACTGTAAAGCTACTTTGTCTACCCCTTCTTCCA 218

Db 557 CTTCTGCGCATCCAAACGCTACTGTCTCATCTGCCATGACGCTTAACACGCTTTTGA 616
QY 219 AGAATTGAACGTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAATAGCAATGG 278
Db 617 AAAGTTAAAGGTTCCCAAGTCCAAAGTCTGTTGTTGCAATTGAATGACATGAAGGAAG 676
QY 279 CTGAGAGATTCAAGAGCTTTAGAAGAAATCTCGGGCCAAAACCTGTACCTTAACGTATA 338
Db 677 CGCAGACATTTCAGGCTCGCTTATGAGATTAAATGGCCAAAGAACCGTGCACAACTCTA 736
QY 339 CATCAATGGCAAGCACATTGCTGTAAACAGCGATTGGAACCTTTGAAGAAAAATGCAAA 398
Db 737 TATTATGTTAAACATATTGGAGGCAACGACGACTTTCAGGAATTTAGGGAGACTGGTGA 796
QY 399 GTTAGCTGAATATTGAAGCCGCTATTTCATA 431
Db 797 ATGGAGGAATTGTAGAACCCTATTCTTGCAA 829

RESULT 7

US-10-932-182A-75707
; Sequence 75707, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 75707
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-75707

Query Match 33.9%; Score 146.6; DB 11; Length 333;
Best Local Similarity 65.3%; Pred. No. 7.8e-31;
Matches 215; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 103 ATGCTATCCAGGAACAGTTGCTCAGTAAAGGATCTGATTGGCCAAAGGAAGTGT 162
Db 1 ATGCTATCTCAAGAACTATCAAGCAGCTCAAGGACCTTATTGCAGAAACGAGATCTTC 60
QY 163 GTTGCAGCAAGACATACTGCCCTTACTGTPAAAGCTACTTTGTCTACCCCTTTCCAAAGAA 222
Db 61 GTCGCATCCAAACGCTACTGTCATCTGCGATGCGCCCTAAACACGCTTTTGAAGAAAG 120
QY 223 TTGAAGCTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAATAGCANTGCTCA 282
Db 121 TTAAGGTTCCCAAGTCCAAAGTCTGTTTTCNAATTGAATGACATGAAGGAAGCGCA 180
QY 283 GAGATTCAAGACGCTTTAGAGAAATCTCGGGCCAAAACCTGTACTTAACGTATACATC 342
Db 181 GACATTCAGGCTGGTTTATGAGATTAAATGGCCAAAGAACCGTGCACAAACATCTATAT 240
QY 343 AATGGCAAGCACATTTGGTGGTAAACAGCGATTGGAACCTTTGAAGAAAAATGCAAGTTA 402
Db 241 AATGGTAAACATATTGAGGCAACGACGATTTCAGGAATTGAGGAGACTGCGCAATTG 300
QY 403 GCTGAATATTGAAGCCGCTATTTCATA 431
Db 301 GAGGAATTGTAGAACCCTATTCTTGCAA 329

RESULT 8

US-10-523-362-1

; Sequence 1, Application US/10523362
; Publication No. US20060064784A1
; GENERAL INFORMATION:
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Puzio, Piotr
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: 536222010300
; CURRENT APPLICATION NUMBER: US/10/523,362
; CURRENT FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; NAME/KEY: CDS
; LOCATION: (1)..(330)
; OTHER INFORMATION: GRX1
US-10-523-362-1

Query Match 33.2%; Score 143.4; DB 12; Length 333;
Best Local Similarity 64.7%; Pred. No. 6.3e-30;
Matches 213; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 103 ATGCTATCCAGGAACAGTTGCTCAGTAAAGGATCTGATTGGCCAAAGGAAGTGT 162
Db 1 ATGCTATCTCAAGAACTATCAAGCAGCTCAAGGACCTTATTTCAGAAAAACGAGATCTTC 60
QY 163 GTTGCAGCAAGACATACTGCCCTTACTGTTAAAGCTACTTTGTCTACCCCTTTCCAAAGAA 222
Db 61 GTCGCATCCAAACGCTACTGTCATCTGCGATGCGCCCTAAACACGCTTTTGAAGAAAG 120
QY 223 TTGAAGCTTCCCAATCCAAAGCCCTTGTGTTGGAATTAGATGAATAGCANTGCTCA 282
Db 121 TTAAGGTTCCCAAGTCCAAAGTCTGTTTTCNAATTGAATGACATGAAGGAAGCGCA 180
QY 283 GAGATTCAAGACGCTTTAGAGAAATCTCGGGCCAAAACCTGTACTTAACGTATACATC 342
Db 181 GACATTCAGGCTGGTTTATGAGATTAAATGGCCAAAGAACCGTGCACAAACATCTATAT 240
QY 343 AATGGCAAGCACATTTGGTGGTAAACAGCGATTGGAACCTTTGAAGAAAAATGCAAGTTA 402
Db 241 AATGGTAAACATATTGAGGCAACGACGACTTCGAGGAATTGAGGAGACTGCTGAATTG 300
QY 403 GCTGAATATTGAAGCCGCTATTTCATA 431
Db 301 GAGGAATTGTAGAACCCTATTCTTGCAA 329

RESULT 9

US-10-032-585-6780
; Sequence 6780, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6780
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-6780

Query Match 20.6%; Score 89; DB 7; Length 360;

Best Local Similarity 55.4%; Pred. No. 1.7e-14;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 67 AGAATTATTCGTAAGAGATTTTATCTACTCCAAAATGTTATCCAGGAAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC 69
QY 127 CAGCTAAAGGATCTGATTTGGCCCAAAAGGAAGTGTGTTGTCAGCAAGACATATCGCCCT 186
Db 70 AAGTCGAACAATTGATCAAAACCAACACCAAGTGTTCATTGCTCCCAATCCTATTGTCCA 129
QY 187 TACTGTAAAGCTACTTGTGCTACCTCTTCCAGAATGTAAGCTTCCCAATCCAAGGCC 246
Db 130 TACTGTAAAGCTACTCAAAAGCAC-----AATTGAAGCTATAACAAAGAGTGTCT 177
QY 247 CTGTGTGTGAATTAGATGAATGAAGCAATGAGCAATGCTCAGAGATTCAAGACGCTTTAGAGAA 306
Db 178 TACAATCTTGAATTAGACGAAGTTGACGAGGTGCTGAAATCCAAAGAGCATTTATTGGAA 237
QY 307 ATCTCGGGCCAAAACCTGTACCTTAACGTATACATCAATGGCAAGCACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAATGTCCTTTATTGGTGGTCAACATATTGGTGGCAAT 297
QY 367 AGCATTTGGAACCTTTGAAAGAAAATGCAAGTTAGCTAGTGAATATTGAAGCCGGTATTT 426
Db 298 TCCGATGTGCAAGCTTTGAAAGTCTAGTGACAAATAGATGACAAAATCAAAGCTGCTTTA 357
QY 427 CAA 429
Db 358 TAA 360

RESULT 10
US-10-451-467A-607
; Sequence 607, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMAN, RIJKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451.467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 607
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-451-467A-607

Query Match 20.6%; Score 89; DB 8; Length 360;
Best Local Similarity 55.4%; Pred. No. 1.7e-14;
Matches 201; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 67 AGAATTATTCGTAAGAGATTTTATCTACTCCAAAATGTTATCCAGGAAACAGTTGCT 126
Db 10 ACATTATTAAACCAAGAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC 69
QY 127 CAGCTAAAGGATCTGATTTGGCCCAAAAGGAAGTGTGTTGTCAGCAAGACATATCGCCCT 186
Db 70 AAGTCGAACAATTGATCAAAACCAACACCAAGTGTTCATTGCTCCCAATCCTATTGTCCA 129
QY 187 TACTGTAAAGCTACTTGTGCTACCTCTTCCAGAATGTAAGCTTCCCAATCCAAGGCC 246

Db 130 TACTGTAAAGGCTACCAAAAGCAC-----AATTGAAGCTATAACAAAGGATGCT 177
QY 247 CTGTGTGTGGAATTAGATGAATGAGCAATGCTCAGAGATTCAAGACGCTTTTAGAAGAA 306
Db 178 TACAATCTTGAATTAGACGAAGTTGACGAGGTGCTGAAATCCAAAGAGCATTTATTGGAA 237
QY 307 ATCTCGGGCCAAAACCTGTACCTTAACGTATACATCAATGGCAAGCACATTTGGTGTAAAC 366
Db 238 ATCACTGGTCAAGAACCGTTCCAATGTCCTTTATTGGTGGTCAACATATTGGTGGCAAT 297
QY 367 AGCATTTGGAACCTTTGAAAGAAAATGCAAGTTAGCTAGTGAATATTGAAGCCGGTATTT 426
Db 298 TCCGATGTGCAAGCTTTGAAAGTCTAGTGACAAATAGATGACAAAATCAAAGCTGCTTTA 357
QY 427 CAA 429
Db 358 TAA 360

RESULT 11
US-10-425-115-146552
; Sequence 146552, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 146552
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(609)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_65172C.1
US-10-425-115-146552

Query Match 14.1%; Score 61; DB 9; Length 609;
Best Local Similarity 63.1%; Pred. No. 1.9e-06;
Matches 94; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 239 CCAAGGCCCTTGTGTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTT 298
Db 312 CAAAGTTCTTACGCGATTGATTTGGACCAAGTTGATGACGCTCAGCTATCCAGTCTACTC 371
QY 299 TAGAAGAAATCTCGGGCCAAAACCTGTACTAAACGTATATACATCAATGCAAGCACATTG 358
Db 372 TCGGCGAAATGACTGGCCAGACCCGCTACCAACATCTTCATCGCTCAGAGCACATTG 431
QY 359 GTGGTAACAGCGATTGGAACCTTTGAAAG 387
Db 432 GTGGAAACAGCGATTGTCAGTCCCAAGAAAG 460

RESULT 12
US-10-425-115-149360
; Sequence 149360, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 149360
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_67741C.1
US-10-425-115-149360

Query Match 13.0%; Score 56; DB 9; Length 377;
Best Local Similarity 53.4%; Pred. No. 3.9e-05;
Matches 147; Conservative 0; Mismatches 115; Indels 12; Gaps 1;

QY 126 TCACGTAAAGGATCTGATTGGCCCAAGGAAGTGTGTGTCAGCAAGACATACCTGCC 185
DB 94 TAAGGTTGCACTGATGATGACAAACGGTGTGTCGTTTCAGCAAGAGCTACTGCC 153
QY 186 TTAAGTGAAGCTACTTTGCTACCTCTTCCAAAGAAATTGAACGTTCCCAAAATCCCAAGGC 245
DB 154 GTACTGCACAAACACGACGCGCTCTC-----GACGGCTACGGTCCCAAGTA 201
QY 246 CCTGTGTTGGAATTAGATGAATAGCAATGGCTCAGAGATTCAAGACGCTTTTGAAGA 305
DB 202 TGCCACGTACGAATGAACAGGAGACGCGGACGACCTCCAGCAGCGCTTGCTCAA 261
QY 306 AATCTGGGCGCAAAACTGTACTACGTATACATCAATGGCAACACATTTGTCGTA 365
DB 262 GATCAGGGCGCAGCGCACGCTCCCAACGCTTCATCAACAAGCAGCATATTGGTGCAA 321
QY 366 CACGCAATTTGAAACTTTGAAGAAAATGGCAAG 399
DB 322 CTCGGACTTGGCGGCTTATTGAACGCGCAAG 355

RESULT 13

US-11-096-568A-26783
; Sequence 26783, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26783
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(578)
; OTHER INFORMATION: Ceres Seq. ID no. 13600582
US-11-096-568A-26783

Query Match 13.0%; Score 56; DB 16; Length 578;
Best Local Similarity 58.3%; Pred. No. 4.8e-05;
Matches 98; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 254 TCGAATTAGTAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCG 313
DB 182 TTGAGTTGGACACTGAAGAGATGGAACATGAGATTGAGTCTGTGTAATGAGACTG 241
QY 314 GCCAAAAAAGCTTACCTTAACGTATACATCAATGGCAAGCACATTTGGTGTAAACAGCGATT 373
DB 242 GGCAGAGACTGTTCCTCAATGTCTTCATCAATGGAACACATTTGGTGGCTGTGACGATA 301

QY 374 TCGAAACTTTGAAGAAAATGCAAGTTAGCTGAAATATTGAAGCCGG 421
DB 302 CTATTGCACTGAACAAGGAGGGAAGCTGGTTGCTCTGCTGACGGAGG 349

RESULT 14

US-10-437-963-29343
; Sequence 29343, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 29343
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_33855C.1
US-10-437-963-29343

Query Match 12.9%; Score 55.6; DB 8; Length 721;
Best Local Similarity 60.7%; Pred. No. 6.9e-05;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 254 TCGAATTAGTGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCG 313
DB 271 TTGAGTTGATGGGAGAGTGTGATCTGAGCTGCGACTTGTGGCTGTGATGATA 330
QY 314 GCCAAAAAAGCTTACCTTAACGTATACATCAATGGCAAGCACATTTGGTGTAAACAGCGATT 373
DB 331 GACAAAGACCTGTTCCAAATGCTTCATCAATGGGAAGCATATTGGTGGCTGTGATGATA 390
QY 374 TCGAAACTTTGAAGAAAATGCAAGTTAG 403
DB 391 CTTGGCATTGAACAATGAAGGGAAGCTGG 420

RESULT 15

US-10-523-362-47
; Sequence 47, Application US/10523362
; Publication No. US20060064784A1
; GENERAL INFORMATION:
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Puzio, Piotr
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Proteins Associated with Abiotic
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: 532622010300
; CURRENT APPLICATION NUMBER: US/10/523,362
; CURRENT FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 47
; LENGTH: 733
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)..(466)
; OTHER INFORMATION: OZ1116C2194
US-10-523-362-47

Query Match	12.9%	Score 55.6;	DB 12;	Length 733;
Best Local Similarity	60.7%;	Pred. No. 7e-05;		
Matches 91; Conservative	0;	Mismatches 59;	Indels 0;	Gaps 0;
Qy	254	TGGAATTTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTTAGAAGAAATCTCGG	313	
Db	258	TTGAGTTGGATGGGAGAGATGGATCTGAGCTGCAGTCGGCACTTCTGATGGACTG	317	
Qy	314	GCCAAAAAACTGTACTTAAGTATACATCAATGGCAGCACTTTGGTGGTAAACAGCGAATT	373	
Db	318	GACAAAGGACTGTTCCAAATGTCTTCATCAATGGAAGCATATTGGTGGCTGTGATGATA	377	
Qy	374	TGGAACCTTTGAAGAAAAATGGCAAGTTAG	403	
Db	378	CTTTGGCATTGAAACAATGGAAGGGAAGCTGG	407	

Search completed: November 7, 2006, 04:05:54
Job time : 1461 secs

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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:08:05 ; Search time 200 Seconds
(without alignments)

326.910 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFDSNLVIVITLF.....DLETLKNGKLAILKPVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*
- 10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	5	ABG93088 S. cerevi
2	714	100.0	143	8	Adk90659 Baker's Y
3	714	100.0	143	8	Adt87075 Yeast Str
4	391	54.8	110	5	ABG93054 S. cerevi
5	391	54.8	110	8	Adk90657 Baker's Y
6	300.5	42.1	119	5	ABG93325 C. albica
7	300.5	42.1	119	5	ABP73943 Candida a
8	216	30.3	136	8	Adk90701 Rice oxid
9	215.5	30.2	127	8	Adk90703 Rice oxid
10	215	30.1	133	3	AGI15306 Arabidops
11	215	30.1	135	3	AGI15305 Arabidops
12	215	30.1	135	8	Adk90687 Thale cre
13	215	30.1	147	3	AGI15304 Arabidops
14	214.5	30.0	133	8	Adk90677 Rape oxid
15	212	29.7	102	8	ADR86373 Aspergill
16	210	29.4	133	3	AGI11727 Arabidops
17	210	29.4	135	3	AGI11726 Arabidops
18	210	29.4	152	3	AGI11725 Arabidops
19	209	29.3	119	5	ABG60108 Human DIT
20	207.5	29.1	173	8	Adk90675 Rape oxid
21	206	28.9	109	3	AG45926 Arabidops
22	206	28.9	109	3	AG09195 Arabidops
23	206	28.9	109	3	AAG06665 Arabidops

24	206	28.9	111	3	AAG09194 Arabidops
25	206	28.9	111	3	AG45925 Arabidops
26	206	28.9	111	3	AG06664 Arabidops
27	206	28.9	111	8	ADK90683 Thale cre
28	204	28.6	120	8	ADK90671 Rape oxid
29	203.5	28.5	122	3	AG04252 Arabidops
30	203.5	28.5	125	3	AG04251 Arabidops
31	203.5	28.5	126	3	AG33583 Arabidops
32	203.5	28.5	129	3	AG33582 Arabidops
33	203	28.4	116	3	AG04253 Arabidops
34	203	28.4	120	3	AG33584 Arabidops
35	199	27.9	109	3	AG35055 Arabidops
36	199	27.9	111	3	AG35054 Arabidops
37	199	27.9	154	3	AG43269 Arabidops
38	199	27.9	169	3	AG43268 Arabidops
39	199	27.9	179	3	AG43267 Arabidops
40	199	27.9	179	8	ADK90689 Thale cre
41	198.5	27.8	122	3	AG46499 Arabidops
42	198.5	27.8	122	3	AG46496 Arabidops
43	198.5	27.8	125	3	AG46498 Arabidops
44	198.5	27.8	125	3	AG46495 Arabidops
45	198	27.7	111	8	ADK90681 Thale cre

ALIGNMENTS

RESULT 1

ABG93088
ID ABG93088 standard; protein; 143 AA.

XX AC ABG93088;

XX DT 21-NOV-2002 (first entry)

XX DE S. cerevisiae BAX-associated protein fragment SEQ ID 134.

XX KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
XX KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
XX KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
XX KW neurodegeneration; cell death.

XX OS Saccharomyces cerevisiae.

XX PN WO200264766-A2.

XX PD 22-AUG-2002.

XX PF 21-DEC-2001; 2001WO-BP015398.

XX PR 22-DEC-2000; 2000EP-00870318.

XX PR 04-JAN-2001; 2001EP-00870002.

XX PR 09-JAN-2001; 2001EP-00870003.

XX PA (JANC) JANSSEN PHARM NV.

XX PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

XX DR WPI; 2002-667002/71.

XX DR N-PSDB; ABQ76354.

XX PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
XX PT medicament for treating, preventing and/or alleviating yeast or fungal
XX PT infections or proliferative disorders, or for preventing apoptosis in
XX PT certain diseases.

XX XX Claim 36; Fig 1; 344pp; English.

XX CC This invention describes a novel nucleic acid representing a synthetic
XX CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
XX CC resistant yeast or fungi, identifying, or obtaining and identifying
XX CC Candida spp. sequences that are differentially expressed in a pathway
XX CC eventually leading to programmed cell death or identifying inhibitors or

CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans or
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC leukaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 714; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1e-71;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGQKEVFVAAKTY 60
DB 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGQKEVFVAAKTY 60
QY 61 CPYCKATLSTLFOELNVPKSKALVLEDEMNSGSEIQDALEEISGQKTPNVYINGKHHG 120
DB 61 CPYCKATLSTLFOELNVPKSKALVLEDEMNSGSEIQDALEEISGQKTPNVYINGKHHG 120
QY 121 GNSDLETLKNGKLAELIKPVFQ 143
DB 121 GNSDLETLKNGKLAELIKPVFQ 143

RESULT 2
ADK90659
ID ADK90659 standard; protein; 143 AA.
XX
AC ADK90659;
XX
DT 20-MAY-2004 (first entry)
XX
DE Baker's yeast glutaredoxin 2 (GRX2) protein SeqID 4.
XX
XX baker's yeast; GRX2; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thiorredoxin; THX; Quantitative Trait Locus; QTL.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2004018687-A2.
XX
PD 04-MAR-2004.
XX
XX 01-JUL-2003; 2003WO-EP006994.
XX
XX 07-AUG-2002; 2002EP-00017671.
XX
XX (BADI) BASF PLANT SCI GMBH.
XX
XX Chardonnens A, Puzio P;
PI Mckersie B, Chen R;
DR WPI: 2004-226856/21.
DR N-PSDB; ADK90659.
XX
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
XX
XX Example 2; SEQ ID NO 4; 140pp; English.

CC This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
CC thiorredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a baker's yeast GRX protein of the invention.
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 714; DB 8; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1e-71;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGQKEVFVAAKTY 60
DB 1 METNFSFDSNLIVIIITLFAIRIIAKRFLSTPKMVSQETVAHVKDILGQKEVFVAAKTY 60
QY 61 CPYCKATLSTLFOELNVPKSKALVLEDEMNSGSEIQDALEEISGQKTPNVYINGKHHG 120
DB 61 CPYCKATLSTLFOELNVPKSKALVLEDEMNSGSEIQDALEEISGQKTPNVYINGKHHG 120
QY 121 GNSDLETLKNGKLAELIKPVFQ 143
DB 121 GNSDLETLKNGKLAELIKPVFQ 143

RESULT 3
ADT87075
ID ADT87075 standard; protein; 143 AA.
XX
AC ADT87075;
XX
DT 13-JAN-2005 (first entry)
XX
DE Yeast Stress-related protein from gene YEL045C.
XX
KW Yeast; Stress-related protein; SRP; environmental stress; abiotic stress;
KW drought; heat; cold; salt.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2004092398-A2.
XX
XX 28-OCT-2004.
XX
XX 15-APR-2004; 2004WO-US011888.
XX
XX 15-APR-2003; 2003EP-00080800.
PR 02-MAY-2003; 2003EP-00039728.
PR 01-AUG-2003; 2003EP-00016672.
PR 30-SEP-2003; 2003EP-00022225.
XX
XX (BADI) BASF PLANT SCI GMBH.
XX
XX Puzio P, Chardonnens A, Shirley A, Wang X, Sarria-Millan R;
PI Mckersie B, Chen R;
XX
XX WPI: 2004-766883/75.
DR N-PSDB; ADT87074.
XX
XX New isolated nucleic acid molecule comprises a sequence encoding Stress-
PT Related Protein (SRP), useful for producing transformed plants with
PT altered metabolic activity resulting in increased tolerance or resistance
PT to environmental stress.
XX

Claim 15; SEQ ID NO 53; 91ppb; English.

The invention relates an isolated nucleic acid molecule comprises a nucleic acid molecule encoding a Stress-Related Protein (SRP) from Yeast or *E. coli* and their homologues from Rice, Soybean and Rape. Also included are a transformed plant cell with altered metabolic activity compared to a corresponding non-transformed wild type plant cell (where the metabolic activity is altered by transformation with a SRP coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell), a transgenic plant generated from the plant cell above (and which is a monocot or dicot plant, or a gymnosperm plant), a seed produced by a transgenic plant above (where the seed is genetically homozygous for a transgene conferring altered metabolic activity resulting in an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant), a nucleic acid construct which confers the expression of the nucleic acid molecule above (comprising one or more regulatory elements, where expression of the SRP coding nucleic acid in a host cell results in altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell), a vector comprising the nucleic acid molecule above or the nucleic acid construct, a host cell which has been transformed stably or transiently with the vector (or the nucleic acid molecules above, or the nucleic acid construct), an isolated Stress Related Protein (SRP) selected from the amino acid sequences fully given in the specification and/or its homologues, a method of producing a transgenic plant with altered metabolic activity compared to a corresponding non-transformed wild type plant cell, modifying stress tolerance of a plant, detecting environmental stress in plant cells or plants, screening plant cells or plants for increased tolerance and/or resistance to environmental stress, breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress, increasing tolerance of a plant to at least one abiotic stress, a plant transformed with the nucleic acids above and a seed of the plant. The altered metabolic activity and/or a SRP encoding nucleic acids or its homologues are useful as markers for selection of plants or plant cells with increased tolerance to environmental stress, or for detection of stress in plants or plant cells. The nucleic acids are useful for producing transformed plants with altered metabolic activity resulting in increased tolerance and/or resistance to an environmental stress (drought, heat, cold and salt) as compared to a corresponding non-transformed wild-type plant cell. The present sequence is a yeast SRP of the invention.

Sequence 143 AA;

Query Match 100.0%; Score 714; DB 8; Length 143;

Best Local Similarity 100.0%; Pred. No. 1.1e-71;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSFDSNLIVIIITLPTATRIIAKRLSTPKMVSQETVAHVKDLIGQKEVFVAAKY 60

DB 1 METNFSFDSNLIVIIITLPTATRIIAKRLSTPKMVSQETVAHVKDLIGQKEVFVAAKY 60

QY 61 CPYCKATLTLFQELNVPKSKALVLELDENSGSEIQDALEEISGQKTPNVVINGKHIG 120

DB 61 CPYCKATLTLFQELNVPKSKALVLELDENSGSEIQDALEEISGQKTPNVVINGKHIG 120

QY 121 GNSDLETLKNGKLAELTKPVFQ 143

DB 121 GNSDLETLKNGKLAELTKPVFQ 143

RESULT 4

ABG93054

ID ABG93054 standard; protein; 110 AA.

XX AC ABG93054;

XX DT 21-NOV-2002 (first entry)

XX DE S. cerevisiae BAX-associated protein fragment SEQ ID 66.

XX

KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death.

XX OS Saccharomycetes cerevisiae.

XX WO200264766-A2.

XX 22-AUG-2002.

XX 21-DEC-2001; 2001WO-EP015398.

XX 22-DEC-2000; 2000EP-00870318.

PR 04-JAN-2001; 2001EP-00870002.

PR 09-JAN-2001; 2001EP-00870003.

XX (JANC) JANSSEN PHARM NV.

PA Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

PI WPI: 2002-667002/71.

XX N-PSDB; ABQ76320.

PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.

XX Claim 36; Fig 1; 34pp; English.

XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX Sequence 110 AA;

Query Match 54.8%; Score 391; DB 5; Length 110;

Best Local Similarity 64.5%; Pred. No. 1.5e-35;

Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 35 MVSQETVAHVKDLIGQKEVFVAAKYCPYCKATLTLFQELNVPKSKALVLELDENSGS 94

DB 1 MVSQETIKHVKDLIAENEIFVASKYCPYCHAAINTLFEKLVKPRSKVLQLNDMKEGA 60

QY 95 EIODALEEISGQKTPNVVINGKHIGNSDLETLKNGKLAELTKPV 141

DB 61 DIOALYEINGQKTPNVVINGKHIGNSDLETLKNGKLAELTKPV 107

RESULT 5

ADK90657

ID ADK90657 standard; protein; 110 AA.

XX AC ADK90657;

XX

DT 20-MAY-2004 (first entry)
XX Baker's yeast glutaredoxin 1 (GRX1) protein SeqID 2.
DE
XX baker's yeast; GRX1; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thioredoxin; THX; Quantitative Trait Locus; QTL.
XX
OS Saccharomyces cerevisiae.
XX
XX WO2004018687-A2.
PN
XX 04-MAR-2004.
PD
XX 01-JUL-2003; 2003WO-EP006994.
PF
XX 07-AUG-2002; 2002EP-00017671.
PR
XX (BADI) BASF PLANT SCI GMBH.
PA
XX Chardonnais A, Puzio P;
PI
XX WPI: 2004-226856/21.
DR N-PSDB; ADK90656.
DR
XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
PT
XX Example 2; SEQ ID NO 2; 140pp; English.
PS
XX This invention relates to novel transgenic plant cells transformed by
XX genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a baker's yeast GRX protein of the invention.
XX
SQ Sequence 110 AA;
Query Match 54.8%; Score 391; DB 8; Length 110;
Best Local Similarity 64.5%; Pred. No. 1.5e-35;
Matches 69; Conservative 23; Mismatches 15; Indels 0; Gaps 0;
QY 35 MVSQETVAHVVDLIGQKEVFAAKTCYPCYKATLSTLFOELNVPKSKALVLELDENSGS 94
DB 1 MVSQETIKHVVDLIGQKEVFAAKTCYPCYKATLSTLFOELNVPKSKALVLELDENSGS 60
QY 95 EIDALVEISGQKTPNVYINGKHIGNSDLETLKNGKLAELIKPV 141
DB 61 DIQAALYEINGQRTVPNVYINGKHIGNSDLETLKNGKLAELIKPV 107
RESULT 6
ABG93325
ID ABG93325 standard; protein; 119 AA.
XX AC ABG93325;
XX DT 21-NOV-2002 (first entry)
XX C. albicans BAX-associated protein fragment SEQ ID 608.
DE
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
• KW

KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death.
XX
OS Candida albicans.
XX WO200264766-A2.
PN
XX 22-AUG-2002.
PD
XX 21-DEC-2001; 2001WO-EP015398.
PF
XX 22-DEC-2000; 2000EP-00870318.
PR 04-JAN-2001; 2001EP-00870002.
PR 09-JAN-2001; 2001EP-00870003.
XX (JANC) JANSSEN PHARM NV.
PA
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
PI WPI: 2002-667002/71.
DR N-PSDB; ABQ76591.
DR
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
PT
XX Claim 36; Fig 2; 344pp; English.
PS
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions, or in
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention
XX
SQ Sequence 119 AA;
Query Match 42.1%; Score 300.5; DB 5; Length 119;
Best Local Similarity 50.4%; Pred. No. 2.5e-25;
Matches 61; Conservative 24; Mismatches 31; Indels 5; Gaps 2;
QY 19 LPATRIIAKRFSLTPKMSQETVAHVVDLIGQKEVFAAKTCYPCYKATLSTLFOELNVP 78
DB 1 MFRT-LLTKRLFTSTMVSSQVKNVQELIKTKPFIASKSYCPYCKATKST----IEAI 55
QY 79 KSKALVLELDENSGSEIQDALLEISGQKTPNVYINGKHIGNSDLETLKNGKLAEL 138
DB 56 TKDAVILELDEVDGAEIQEALLETITGQRTVPNVFVGQHQHIGNSDVQALKSKDLDDKI 115
QY 139 K 139
DB 116 K 116
RESULT 7
ABP73943
ID ABP73943 standard; protein; 119 AA.

Db 71 EPPVVELDQEDGWEIQDALSDMVGRRTVPQVFHGHGLGSDDTVEAYESGKLAKLL 128

RESULT 9
ADK90703
ID ADK90703 standard; protein; 127 AA.

AC ADK90703;

XX 20-MAY-2004 (first entry)

XX Rice oxidoreductase stress-related protein O21116C2194 SeqID 48.

DE rice; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thiorredoxin; THX; Quantitative Trait Locus; QTL.

XX Oryza sativa.

XX WO2004018687-A2.

XX 04-MAR-2004.

XX 01-JUL-2003; 2003WO-EP006994.

XX 07-AUG-2002; 2002EP-00017671.

XX (BADI) BASF PLANT SCI GMBH.

XX Chardonnais A, Puzio P;

XX WPI; 2004-226856/21.

XX N-PSDB; ADK90702.

XX New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.

XX Example 2; SEQ ID NO 48; 140pp; English.

XX This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thiorredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a rice ORSRP protein of the invention.

XX Sequence 127 AA;

Query Match 30.2%; Score 215.5; DB 8; Length 127;
Best Local Similarity 43.0%; Pred. No. 9.7e-16;
Matches 49; Conservative 19; Mismatches 41; Indels 5; Gaps 3;

QY 25 IAKRFILSTPKMVSQETVAHVKDLIGQKEVFAAKTYCPYCKATLSTLFOELNVPKSKALV 84

DB 3 IASSSSSTPS-RKMAKAKETVAGAPVVVYSKSPCPFC-VRVKKLFEQLG---ATFKA 57

QY 85 LEIDEMNSGEIQDALEELSGQTVNVYNGHIGNSDLETLLKNGKLAETL 138

DB 58 IELDGSDELSQSLAEAWTGQRTVPNVFINGKHIGGCDTTLALNNEGKLVPLL 111

RESULT 10
AAG15306

ID AAG15306 standard; protein; 133 AA.
XX AAG15306;
AC AAG15306;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 15509.
DE Arabidopsis thaliana.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
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XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
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XX 23-APR-1999; 99US-0130510P.
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XX 30-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 04-MAY-1999; 99US-0132407P.
XX 05-MAY-1999; 99US-0132484P.
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XX 24-MAY-1999; 99US-0135629P.
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PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.

PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
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PR 20-SEP-1999; 99US-0154039P.
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PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 05-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 12-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.1%; Score 215; DB 3; Length 133;
Best Local Similarity 38.3%; Pred. No. 1.2e-15;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;
QY 7 FDSNLVITITLPAIRIAKRFSLTPKMWQBTVAHVXDLICQKEVFAAKTYCPYCKA 66
Db 2 FRISIMVLLVALVTFTISMVSSAASPE-----ADFKVKTITSHKIVIPSKSYCPYCKK 55
QY 67 TLSTLFOELN-VPKSKALVLELDEMNGSEIQDALEEIISQKTVPNVYINGKHIGNSDL 125
Db 56 AKS-VFRELDQVB-----YVVELDEREDGWSIQTALGEIVGRRTVPQVFINGRHLGGSDDT 110
QY 126 ETLKNGKLAAIL 138
Db 111 VDAYSGBELAKLL 123

RESULT 11
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
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PR 31-AUG-1999; 99US-0151438P.
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PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
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PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
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PR 28-SEP-1999; 99US-0156458P.
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PR 04-OCT-1999; 99US-0157117P.
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 22-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.18; Score 215; DB 3; Length 147;
Best Local Similarity 38.34; Pred. No. 1.4e-15;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;

QY 7 FDSNLIVIIITLIPATRIIAKRLFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTVCYCKA 66
DB 16 FRISWMLVALVTFISMVSSAASPE-----ADFVKTTISHKIVIFSCKYCPYCKK 69
QY 67 TLSTLFOELN-VPKSKALVLELDEMNSGSIQDALEISQKTVPNVYINGKHIGNSDL 125
DB 70 AKS-VPELQVPH---YVVELDEREDGWSIQTALGSEIVGRTRTPQVFINGKLGGSDDT 124
QY 126 ETLKNGKLAAIL 138
DB 125 VDYESGELAKLL 137

us-10-523-362-4.rag

RESULT 14
ADK90677
ID ADK90677 standard; protein; 133 AA.
XX
AC ADK90677;
XX
DT 20-MAY-2004 (first entry)
XX
DE Rape oxidoreductase stress-related protein BN1106C2582 SeqID 22.
XX
KW rape; transgenic; abiotic stress response; crop plant;
KW oxidoreductase stress-related protein; ORSRP; environmental stress;
KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
KW thioredoxin; THX; Quantitative Trait Locus; QTL.
XX
OS Brassica napus.
XX
PN W02004018687-A2.
XX
PD 04-MAR-2004.
XX
PF 01-JUL-2003; 2003WO-EP06994.
XX
PR 07-AUG-2002; 2002EP-00017671.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Chardonnais A, Puzio P;
XX
PP WPI; 2004-226856/21.
XX
DR N-PSDB; ADK90676.
XX
PT New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
PT plant with increased environmental stress tolerance.
XX
PS Example 2; SEQ ID NO 22; 140pp; English.
XX
CC This invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/ or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/ or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a rape ORSRP protein of the invention.
XX
SQ Sequence 133 AA;

Query Match 30.0%; Score 214.5; DB 8; Length 133;
Best Local Similarity 36.7%; Pred. No. 1.3e-15;
Matches 51; Conservative 30; Mismatches 41; Indels 17; Gaps 5;

QY 1 METNFSFDSNLIVIIITLIPATRIIAKRLFLSTPKMVSQETVAHVKDLIGQKEVFVAAKT 60
DB 3 MMSFSFDSNLIVIIITLIPATRIIAKRLFLSTPKMVSQETVAHVKDLIGQKEVFVAAKT 51
QY 61 CPYCKATLSTLFOELN-VPKSKALVLELDEMNSGSIQDALEISQKTVPNVYINGKHI 119
DB 52 CPYCKATLSTLFOELN-VPKSKALVLELDEMNSGSIQDALEISQKTVPNVYINGKHI 106
QY 120 GNSDLETLKNGKLAAIL 138
DB 107 GGSDDTVTAHESGELAKLL 125

RESULT 15
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 03:36:27 ; Search time 182 Seconds
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4605.624 Million cell updates/sec

Title: US-10-523-362-3
Perfect score: 432
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Scoring table: IDENTITY NUC
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Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters: 4922752

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
1: /EMC Celleria_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:
2: /EMC Celleria_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:
3: /EMC Celleria_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:
4: /EMC Celleria_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:
5: /EMC Celleria_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:
6: /EMC Celleria_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:
7: /EMC Celleria_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:
8: /EMC Celleria_SIDS3/ptodata/1/pubpna/US12_NEW_PUB.seq:
9: /EMC Celleria_SIDS3/ptodata/1/pubpna/US13_NEW_PUB.seq:
10: /EMC Celleria_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	432	100.0	432	8	US-11-217-529-76174
2	432	100.0	432	8	US-11-251-208-52
3	336.6	77.9	570	8	US-11-217-529-3898
4	153.8	35.6	345	8	US-11-217-529-3588
5	146.6	33.9	333	8	US-11-217-529-75707
6	56	13.0	578	6	US-10-953-349-37584
7	55.6	12.9	575	6	US-10-449-902-15440
8	55.6	12.9	729	6	US-10-449-902-4892
9	55	12.7	392	6	US-10-449-902-279
10	55	12.7	885	9	US-11-218-305-2985
11	53.2	12.3	597	8	US-11-216-545-6672
12	49.4	11.4	568	6	US-10-953-349-14823
13	49.2	11.4	695	6	US-10-953-349-20411
14	49.2	11.4	894	9	US-11-218-305-4450
15	47.2	10.9	790	6	US-10-449-902-17381
16	47	10.9	282	8	US-11-217-529-79774
17	46.8	10.8	385	7	US-11-314-834-1485
18	46.8	10.8	590	7	US-11-292-078-8409
19	46.4	10.7	529	7	US-11-314-834-628
20	45.6	10.6	844	9	US-11-218-305-2209
21	45	10.4	550	7	US-11-292-078-16761
22	44.8	10.4	693	6	US-10-953-349-28950
23	43.8	10.1	343	7	US-11-292-078-4027

ALIGNMENTS

RESULT 1
US-11-217-529-76174
; Sequence 76174, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIOHRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76174
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76174

Query Match 100.0%; Score 432; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.6e-120;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACCAATTTTTCCTTCGACTCGAATTTAATTTGTTTATTTATCATTTACCGTCTTTT 60
Db 1 ATGAGACCAATTTTTCCTTCGACTCGAATTTAATTTGTTTATTTATCATTTACCGTCTTTT 60

QY 61 GCCACAAGAAATTTGCTAAAAGATTTTATCTACTCCAAAATTTGTTATCCAGGAACA 120
Db 61 GCCACAAGAAATTTGCTAAAAGATTTTATCTACTCCAAAATTTGTTATCCAGGAACA 120

QY 121 GTTGCTCAGTAAGGATCTGATGGCCAAAGAGATGTTGTTGTCAGCAAGACATAC 180
Db 121 GTTGCTCAGTAAGGATCTGATGGCCAAAGAGATGTTGTTGTCAGCAAGACATAC 180

QY 181 TGGCCTTACTGTAAGCTACTTTGTTCTACCTCTTCCAGAAATTTGACGTTCCCAATCC 240
Db 181 TGGCCTTACTGTAAGCTACTTTGTTCTACCTCTTCCAGAAATTTGACGTTCCCAATCC 240

QY 241 AAGGCCCTTGTGTGGAAATAGATGAAATGAGCAATGGCTCAGAGATTCAAGCGCTTTA 300

Sequence 2381, Ap
Sequence 3957, Ap
Sequence 2766, Ap
Sequence 4451, Ap
Sequence 10453, A
Sequence 368174, A
Sequence 389005, A
Sequence 451553, A
Sequence 128973, A
Sequence 128973, A
Sequence 228835, A
Sequence 243133, A
Sequence 243133, A
Sequence 345333, A
Sequence 503, App
Sequence 8854, Ap
Sequence 5650, Ap
Sequence 5422, Ap
Sequence 2210, Ap
Sequence 367899, A
Sequence 451278, A
Sequence 23227, A

|||||
Db 241 AAGGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
QY 301 GAAGAAATCTCGGCCCAAAAACCTGTACTTAACGTATACATCAATGCGCAAGCATTGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACCTGTACTTAACGTATACATCAATGCGCAAGCATTGGT 360
QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Db 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
QY 421 GTATTTCATATAG 432
Db 421 GTATTTCATATAG 432

RESULT 3
US-11-251-208-52
; Sequence 52, Application US/11251208
; Publication No. US20060137043A1
; GENERAL INFORMATION:
; APPLICANT: Puzio, Piotr
; APPLICANT: Chardonnens, Agnes
; APPLICANT: Shirley, Amber
; APPLICANT: Wang, Xi-Qing
; APPLICANT: Sarria-Millen, Rodrigo
; APPLICANT: McKersie, Bryan
; APPLICANT: Chen, Ruoying
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
; FILE REFERENCE: 13311-00015-US
; CURRENT APPLICATION NUMBER: US/11/251,208
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: PCT/US2004/011888
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: EP 03008080.8
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: EP 03009728.1
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: EP 03016672.2
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: EP 03022225.1
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
US-11-251-208-52

Query Match 100.0%; Score 432; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.6e-120;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGACCAATTTTCCCTCGACTCGAATTTAAATTTGTTATTATCATTTACGTTGTTT 60
Db 1 ATGGAGACCAATTTTCCCTCGACTCGAATTTAAATTTGTTATTATCATTTACGTTGTTT 60
QY 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 120
Db 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 120
QY 121 GTTGCTCAGTAAAGATCTGATTGGCCAAAAGAAAGTGTGTTGTCGACGAAGACATAC 180
Db 121 GTTGCTCAGTAAAGATCTGATTGGCCAAAAGAAAGTGTGTTGTCGACGAAGACATAC 180
QY 181 TGCCTTACTGTAAAGCTACTTTGTCTACCTCTTCCAAAGAATTTGAACGTTCCCAATCC 240
|||||

Db 181 TGCCTTACTGTAAAGCTACTTTGTCTACCTCTTCCAAAGAATTTGAACGTTCCCAATCC 240
QY 241 AAGGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 241 AAGGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
QY 301 GAAGAAATCTCGGCCCAAAAACCTGTACTTAACGTATACATCAATGCGCAAGCATTGGT 360
Db 301 GAAGAAATCTCGGCCCAAAAACCTGTACTTAACGTATACATCAATGCGCAAGCATTGGT 360
QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
Db 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420
QY 421 GTATTTCATATAG 432
Db 421 GTATTTCATATAG 432

RESULT 3
US-11-217-529-3898
; Sequence 3898, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3898
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3898

Query Match 77.9%; Score 336.6; DB 8; Length 570;
Best Local Similarity 86.3%; Pred. No. 1.7e-91;
Matches 372; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 ATGGAGACCAATTTTCCCTCGACTCGAATTTAAATTTGTTATTATCATTTACGTTGTTT 60
Db 139 ATGGAAACTAAATTTTCTTTCGACTCAAAATTTAATCGTTATTGTCATTTACGTTGTTT 198
QY 61 GCCACAAGAAATTTGCTAAAGATTTTATCTACTCCAAAATGGTATCCCAAGGAAACA 120
Db 199 GCCACCAGAAATTTATCGCTAAAGATTTTATCTACTCCCAAAAATGGTATCTCAAGAAACA 258
QY 121 GTTGCTCAGTAAAGATCTGATTGGCCAAAAGGAGTGTGTTGTCGACGAAGACATAC 180
Db 259 ATTGCACACGTAAGAGACTTGTATTGGCCAAAAGAGGCTCTCGTTTGGCGGAGACATAC 318
QY 181 TGCCTTACTGTAAAGCTACTTTGTCTACCTCTTCCAAAGAATTTGAACGTTCCCAATCC 240
Db 319 TGTCTTACTGTAAAGCCACATTTGCCCTTGTTCAGGAATTTGACGTTTCTTAATCC 378
QY 241 AAGGCCCTTGTGTGGAAATAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTA 300
Db 379 AAGCCGTTGTTTGGAGTTGGACGAATGGATGGTTCAGAAATCCAGGATGCTCTC 438
QY 301 GAAGAAATCTCGGCCCAAAAACCTGTACTTAACGTATACATCAATGCGCAAGCATTGGT 360
Db 439 GAAGAAATTTCCGGGCCAAAAGAACTGTACTCAAAACGTTTACATCAATGGTGAAGCATTCCG 498
QY 361 GGTAAACAGCGATTGGAACTTTGAAGAAAATGGCAAGTTAGCTGAAATATTGAAGCCG 420

Db 499 GGAACAGCGATTTCGAAGCTTTCGAAGAAAACGGTAAATTGGCTGAATATTATTGAAACCG 558
Qy 421 GTATTTCATA 431
Db 559 GTTTTCGAATA 569

RESULT 4

```

US-11-217-529-3588
; Sequence 3588, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3588
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3588

```

DEFINITION 5

Query Match	Best Local Similarity	Mismatches	Indels	Gaps	Length
13.0%	58.3%	0	70	0	378
Match	Conservative				
254	TGGAATTAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTTGAAGAATACTCGG	313			
Db	182	TTGAGTTGCACACTGAAGCGATGGAACCTGAGATTCAGTCAGCTCTTCTGCTGAATGGACTG	241		
Qy	314	GCACAAAACTGTACTACGTATACATCAATGGCAAGCAATTTGGTGGTAAACAGCATTT	373		
Db	242	GGCAGAGGACTCTTCCCAATGTCTTCAATCAATGGAACACATTTGGTGGTGAACGCGATA	301		
Qy					
Db					

QY 374 TGAACCTTTGACAAATAATGGCAAGTAGCTGAAATATTTGAAGCGG 421
DB 302 CTATTGCACTGAACAAAGGGGAGGAAGCTGTTGCTCTGCTGACGGAGG 349

RESULT 7

US-10-449-902-15440
; Sequence 15440, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15440

; LENGTH: 575

; TYPE: DNA

; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: AK065962

; DATABASE ENTRY DATE: 2001-12-06

US-10-449-902-15440

Query Match 12.9%; Score 55.6; DB 6; Length 575;
Best Local Similarity 60.7%; Pred. No. 9 6e-07;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 254 TGAATTTAGTAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAATCTCGG 313

DB 172 TTGAGTTGGATGGGAGAGATGATGATCTGAGCTGCGGACCTTGCTGAATGGACTG 231

QY 314 GCCAAAACTGTACTTAAGTATACATCATGTCGCAAGCACATTTGGTGGTACAGCGATT 373

DB 232 GACAAAGGACTGTTCCTCAATGTCTTCAATGGGAAGCATATTGGTGGCTGTGATGATA 291

QY 374 TGAACCTTTGACAAATAATGGCAAGTAGCTGAAATATTTGAAGCGG 403

DB 292 CTTTGGCATTGAACATGAAGGGAAGCTGG 321

RESULT 8

US-10-449-902-4892
; Sequence 4892, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4892

; LENGTH: 729

; TYPE: DNA

; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK062117
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-4892

Query Match 12.9%; Score 55.6; DB 6; Length 729;
Best Local Similarity 60.7%; Pred. No. 1.1e-06;
Matches 91; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 254 TGAATTTAGTAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAATAATCTCGG 313

DB 326 TTGAGTTGGATGGGAGAGATGATGATCTGAGCTGCGGACCTTGCTGAATGGACTG 385

QY 314 GCCAAAACTGTACTTAAGTATACATCAATGCGCAAGCACATTTGGTGGTAAACAGCGATT 373

DB 386 GACAAAGGACTGTTCCTCAATGTCTTCAATGGGAAGCATATTGGTGGCTGTGATGATA 445

QY 374 TGAACCTTTGACAAATAATGGCAAGTAGCTGAAATATTTGAAGCGG 403

DB 446 CTTTGGCATTGAACATGAAGGGAAGCTGG 475

RESULT 9

US-10-449-902-279
; Sequence 279, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 279

; LENGTH: 392

; TYPE: DNA

; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: AK058431

; DATABASE ENTRY DATE: 2001-12-06

US-10-449-902-279

Query Match 12.7%; Score 55; DB 6; Length 392;
Best Local Similarity 57.1%; Pred. No. 1.2e-06;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 242 AGCCCTTGTGTTGGAATTAGATGAATAAGAGCAATGGCTCAGAGATTCAAGACGCTTTAG 301

DB 36 AGCCCTATGTTTGTGGAGCTTGATCAACGAGAGGATGGTTGGGAGATTCAAGATGCCCTTAT 95

QY 302 AGNAATCTCGGGCCAAAAAACTGTACTTAAGTATACATCAATGCGCAAGCACATTGGTG 361

DB 96 CTGACATGTTGGCAGGCAACTGTCTTCAAGTTTTTGTCCATGGGAAGCACCTGGTG 155

QY 362 GTACACAGCGATTGGAAACTTTTGAAGAAAAATGGCAAGTTAGCTGAATATTGAA 416

DB 156 GCTCTGATGATCTGTTGAAGCATATGAGAGTGGCAAGCTAGCCAAACTTTTGAA 210

RESULT 10

US-11-218-305-2985

; Sequence 2985, Application US/11218305

; Publication No. US20060141495A1

; GENERAL INFORMATION:

; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; PRIOR FILING DATE: 2005-09-01
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2985
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-2985

Query Match 12.7%; Score 55; DB 9; Length 885;
Best Local Similarity 57.1%; Pred. No. 1.7e-06;
Matches 100; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 242 AGCCCTTGTGGATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAG 301
DB 363 AGCATATGTTGGAGCTTGATGACGAGAGGATGGCTCAGAGATTCAAGATTCAGCTTAC 422
QY 302 AAGAAATCTCGGGCAAAAACTGTACTAACTATATACATCAATGCAAGCACATTTGGTG 361
DB 423 TTGATAGTTGGCAGCGTACTGCTCAAGTTTGTGCTGGAAGCACCTGGTG 482
QY 362 GTAACAGCGATTGGAACTTTGAAGAAAAATGCAAGTTAGCTGAAATTTGAA 416
DB 483 GTTCTGACGACTGTTGACTCTCTACGAAAGTGGAATACTGGCTAGACTTCTAAA 537

RESULT 11
US-11-216-545-6672
; Sequence 6672, Application US/11216545
; Publication No. US20060135758A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53659)B
; CURRENT APPLICATION NUMBER: US/11/216,545
; CURRENT FILING DATE: 2005-08-31
; PRIOR FILING DATE: 2005-08-31
; PRIOR FILING DATE: 2004-08-31
; NUMBER OF SEQ ID NOS: 8783
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6672
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Glycine max
US-11-216-545-6672

Query Match 12.3%; Score 53.2; DB 8; Length 597;
Best Local Similarity 58.0%; Pred. No. 5.2e-06;
Matches 94; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 254 TGGATTAGTGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGG 313
DB 172 TTGATTGGACACTGAAAGCGATGGAACCTGAGATTCAAGTTCAGCTCTTGTGTAATGGACTG 231
QY 314 GCCAAAAAATCTGTACTTAACGTATACATCAATGCAAGCACATTTGGTGGTAAACAGCGATT 373

DB 232 GCAGAGGACTGTTCCCAATGTCTTCATCAATGAAAAACACATCGGTGGTGTGACGATA 291
QY 374 TGGAACTTTTGAAGAAAAATGCAAGTTAGCTGAAATATTGA 415
DB 292 CTATTGCACTGAACAAGGAGGAAGCTGTTGCTCTGTCTGA 333
RESULT 12
US-10-953-349-14823
; Sequence 14823, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14823
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-14823

Query Match 11.4%; Score 49.4; DB 6; Length 568;
Best Local Similarity 54.7%; Pred. No. 7.1e-05;
Matches 98; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 237 ATCCAAGGCCCTTGTGTGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGC 296
DB 186 AGCTAATTATCGCCGTTGAGCTCGCAAGAGAGTGATGGTAGCAAGTTCAATCAGC 245
QY 297 TTTAGAGAAATCTCGGGCCAAAAAATGTACTTAAGTATATACATCAATGGCAAGCAT 356
DB 246 TCTGGCAGAAATGACAGAGACACGCCCTGTCCCAATGTGTTCATAGGTGAAAAACACAT 305
QY 357 TGGTGGTAAACAGCGATTTCGAACTTTGAAGAAAAATGCAAGTTAGCTGAAATATTGA 415
DB 306 CGGTGGCTGGATTCTGTAAACAACCTGCACAGAGAGCGCAAGTTGTTCTTATATTGA 364

RESULT 13
US-10-953-349-20411
; Sequence 20411, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20411
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20411

Query Match 11.4%; Score 49.2; DB 6; Length 695;
Best Local Similarity 58.0%; Pred. No. 8.9e-05;
Matches 87; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 254 TGGAAATTAGATGAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAGAAATCTCGG 313
DB 184 TTGATTGGATGAAGGAAGTATGAGCTGAGCTCCAGATGCGCTGAAGAGTGGACTG 243
QY 314 GCCAAAAAATCTGTACCTTAACGTATACATCAATGCAAGCACATTTGGTGGTAAACAGCGATT 373

Db 244 GACAGGAGCTGTCCCAATGTCTTCATCAATGGAGCATATTGGGGCTGTGATGATA 303

QY 374 TGGAAACTTTGAAGAAAAATGGCAAGTTAG 403

Db 304 CTATGGCACTGAACAATGATGGGAAGCTGG 333

RESULT 14

US-11-218-305-4450
; Sequence 4450, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McAlaird, Paul L.
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4450
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-4450

Query Match 11.4%; Score 49.2; DB 9; Length 894;
Best Local Similarity 58.0%; Pred. No. 9.8e-05;
Matches 87; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 254 TGGAACTAGTAAGTAAGCAATGGCTCAGAGATTCAGACGCTTTAGAGAAATCTCGG 313

Db 327 TTGAGTTGGATAAGGAAGATGATGGAGCTGAGCTCCAGAAATGCCCTGAAGGAGTGGACTG 386

QY 314 GCCAAAAACTGTACCTAACGTATACATCAATGGCAAGCACATTTGGTGGTAACAGCGATT 373

Db 387 GACAGGAGCTGTCCCAATGTCTTCATCAATGGGAAGCATATTGGGGCTGTGATGATA 446

QY 374 TGGAAACTTTGAAGAAAAATGGCAAGTTAG 403

Db 447 CTATGGCACTGAACAATGATGGGAAGCTGG 476

RESULT 15

US-10-449-902-17381
; Sequence 17381, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17381
; LENGTH: 790
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK067828

; DATABASE ENTRY DATE: 2001-12-06

US-10-449-902-17381

Query Match 10.9%; Score 47.2; DB 6; Length 790;
Best Local Similarity 53.9%; Pred. No. 0.00037;
Matches 97; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 222 ATTGAACGTTCCCAATCCAAGGCCCTTGTGTTGGAAATTAGATGAATGAGCAATGGCTC 281

Db 251 ATTTAGAGATCTCAAGGAGATCCTTATATTGTTGAACCTAGATCTCAGAGAGGATGGTAG 310

QY 282 AGAGATTCAAGACGCTTTTAGAAGAAATCTCGGGCCCAAAAACTGTACCTAAACGTATACAT 341

Db 311 AGAAATTCAAAGTGTCTTCTTAGACTTTAGTTGGCCGCTCATCTGTGCCACAGGTGTCTGT 370

QY 342 CAATGGCAAGCACATTTGGTGGTAACAGCGATTTTGGAACCTTTTGAAGAAAAAATGGCAAGTT 401

Db 371 GAATGGCCAGCACGTTGGTGGCTCAGATGATACAGCAATGCTCATTTCTAATGGACAGCT 430

Search completed: November 7, 2006, 03:39:38
Job time : 184 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 6, 2006, 19:19:05 ; Search time 41 Seconds
(without alignments)
292.088 Million cell updates/sec

Title: US-10-523-362-4

Perfect score: 714

Sequence: 1 METNFSFSDSLVILITL.....DLTLKNGKLALPKVFQ 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 320231 seqs, 83745634 residues

Total number of hits satisfying chosen parameters: 320231

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.psp.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.psp.*
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- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.psp.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.psp.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	714	100.0	143	7	US-11-251-208-53
2	223	31.2	135	6	US-10-953-349-28952
3	223	31.2	166	6	US-10-953-349-28951
4	218.5	30.6	131	6	US-10-953-349-37585
5	215.5	30.2	155	6	US-10-449-902-33357
6	215	30.1	113	6	US-10-953-349-37586
7	215	30.1	133	6	US-10-953-349-5626
8	215	30.1	135	6	US-10-953-349-5625
9	215	30.1	152	6	US-10-953-349-5624
10	209	29.3	112	6	US-10-449-902-43865
11	209	29.3	113	6	US-10-953-349-20413
12	209	29.3	131	6	US-10-953-349-20412
13	206	28.9	109	6	US-10-953-349-8856
14	206	28.9	111	6	US-10-953-349-8855
15	203	28.4	102	7	US-11-317-789A-854
16	199	27.9	109	6	US-10-953-349-14825
17	199	27.9	111	6	US-10-953-349-14824
18	185.5	26.0	131	6	US-10-449-902-45793
19	179.5	25.1	613	6	US-10-952-500-302
20	169.5	23.7	164	6	US-10-449-902-33706
21	160	22.4	579	6	US-10-952-500-294
22	159	22.3	577	6	US-10-952-500-296
23	128	17.9	100	6	US-10-953-349-4116
24	128	17.9	102	6	US-10-953-349-4115
25	127	17.8	96	6	US-10-953-349-4117

26	124.5	17.4	103	6	US-10-953-349-10133	Sequence 10133, A
27	124.5	17.4	108	7	US-11-291-305-83	Sequence 83, Appl
28	118.5	16.6	103	6	US-10-449-902-38965	Sequence 38965, A
29	118.5	16.6	103	7	US-11-317-789A-851	Sequence 851, App
30	110.5	15.5	119	7	US-11-056-355B-10140	Sequence 10140, A
31	110.5	15.5	130	7	US-11-056-355B-10139	Sequence 10139, A
32	108	15.1	105	6	US-10-953-349-15523	Sequence 15523, A
33	108	15.1	136	6	US-10-953-349-15522	Sequence 15522, A
34	106.5	14.9	113	7	US-11-056-355B-10141	Sequence 10141, A
35	103.5	14.5	236	7	US-11-056-355B-79862	Sequence 79862, A
36	103.5	14.5	239	7	US-11-056-355B-79861	Sequence 79861, A
37	102	14.3	318	7	US-11-056-355B-79263	Sequence 79263, A
38	102	14.3	385	7	US-11-056-355B-97262	Sequence 97262, A
39	102	14.3	428	7	US-11-056-355B-97261	Sequence 97261, A
40	100	14.0	81	6	US-10-953-349-10135	Sequence 10135, A
41	100	14.0	108	6	US-10-449-902-39122	Sequence 39122, A
42	100	14.0	140	6	US-10-953-349-6594	Sequence 6594, Ap
43	100	14.0	166	6	US-10-953-349-6593	Sequence 6593, Ap
44	99	13.9	104	6	US-10-449-902-34921	Sequence 34921, A
45	99	13.9	121	6	US-10-953-349-6595	Sequence 6595, Ap

ALIGNMENTS

RESULT 1

US-11-251-208-53

; Sequence 53, Application US/11251208

; Publication No. US20060137043A1

; GENERAL INFORMATION:

; APPLICANT: Puzio, Piotr

; APPLICANT: Chardonnens, Agnes

; APPLICANT: Shirley, Amber

; APPLICANT: Wang, Xi-Qing

; APPLICANT: Sarria-Millan, Rodrigo

; APPLICANT: Mckersie, Bryan

; APPLICANT: Chen, Ruoying

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED TOLERANCE TO ENVIRONMENTAL STRESS

; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS

; FILE REFERENCE: 13311-00015-US

; CURRENT APPLICATION NUMBER: US/11/251,208

; CURRENT FILING DATE: 2005-10-14

; PRIOR APPLICATION NUMBER: PCT/US2004/011888

; PRIOR FILING DATE: 2004-04-15

; PRIOR APPLICATION NUMBER: EP 03008080.8

; PRIOR FILING DATE: 2003-04-15

; PRIOR APPLICATION NUMBER: EP 03009728.1

; PRIOR FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: EP 03016672.2

; PRIOR FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: EP 03022225.1

; PRIOR FILING DATE: 2003-09-30

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: Patent in version 3.3

; SEQ ID NO 53

; LENGTH: 143

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-11-251-208-53

Query Match 100.0%; Score 714; DB 7; Length 143;

Best Local Similarity 100.0%; Pred. No. 2e-58;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METNFSFSDSLVILITLPTATRIIAKRFLLSTPKMSQETVAHVKOLIGQKVFVAAKTY 60

Db 1 METNFSFSDSLVILITLPTATRIIAKRFLLSTPKMSQETVAHVKOLIGQKVFVAAKTY 60

Qy 61 CPYCKATLSTLFOELNVPKSKALVLELDENSGSEIQTDALEESIGOKTVPNVYINGKHIG 120

Db 61 CPYCKATLSTLFOELNVPKSKALVLELDENSGSEIQTDALEESIGOKTVPNVYINGKHIG 120

QY 121 GNSDLETLKNGKLAELKPVFQ 143
Db 121 GNSDLETLKNGKLAELKPVFQ 143

RESULT 2

US-10-953-349-28952
; Sequence 28952, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28952
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28952

Query Match 31.2%; Score 223; DB 6; Length 135;
Best Local Similarity 38.8%; Pred. No. 2.5e-13;
Matches 47; Conservative 25; Mismatches 45; Indels 4; Gaps 3;

QY 20 FTRIITAKRFLSTPKM--VSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNV 77
Db 9 FSVAAAAAFIALAAGSASASTAFVKSTVKAHDVVFVSKSCPYCKRA-KAVFKELEL 67
QY 78 PKSKALVLEDEMSNGSEIQDALEEISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 137
Db 68 -KXDPYVVELDQEDGGEIQDALSDMVGRRTVPQVFIRGKHLGSGDDTVDAYENGELAKL 126
QY 138 L 138
Db 127 L 127

RESULT 3

US-10-953-349-28951
; Sequence 28951, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28951
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28951

Query Match 31.2%; Score 223; DB 6; Length 166;
Best Local Similarity 38.8%; Pred. No. 3.2e-13;
Matches 47; Conservative 25; Mismatches 45; Indels 4; Gaps 3;

QY 20 FTRIITAKRFLSTPKM--VSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNV 77
Db 40 FSVAAAAAFIALAAGSASASTAFVKSTVKAHDVVFVSKSCPYCKRA-KAVFKELEL 98
QY 78 PKSKALVLEDEMSNGSEIQDALEEISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 137
Db 99 -KXDPYVVELDQEDGGEIQDALSDMVGRRTVPQVFIRGKHLGSGDDTVDAYENGELAKL 157
QY 138 L 138

Db 158 L 158

RESULT 4

US-10-953-349-37585
; Sequence 37585, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 37585
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37585

Query Match 30.6%; Score 218.5; DB 6; Length 131;
Best Local Similarity 44.4%; Pred. No. 6.2e-13;
Matches 48; Conservative 19; Mismatches 36; Indels 5; Gaps 3;

QY 31 STPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALVLEDEM 90
Db 12 STPEGRAM-ALAKAKEIVASAPVWFSKSYCPFC-VQVKKLFQLG---ASFKAIELDTE 66
QY 91 SNGSEIQDALEEISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 138
Db 67 SDGTETQSALAEWTGQRTVPNPVFNFGKHIGGCGDDTIALNKGKGLVALL 114

RESULT 5

US-10-449-902-33357
; Sequence 33357, Application US/10449902
; Publication No. US20060123505A1

GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33357
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33357

Query Match 30.2%; Score 215.5; DB 6; Length 155;
Best Local Similarity 43.0%; Pred. No. 1.4e-12;
Matches 49; Conservative 19; Mismatches 41; Indels 5; Gaps 3;

QY 25 IAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLSTLFOELNVPKSKALV 84
Db 31 IASSSSSTPES-RKALAKAKETVASAPVVVTSKSYCPFC-VRVKKLFEQLG---ATFKA 85
QY 85 LBLDEMSNGSEIQDALEEISGQKTPVNPVYINGKHIGGNSDLETLKNGKLAEL 138
Db 86 IELDGSDGSELQSALEWTGQRTVPNPVFNFGKHIGGCGDDTIALNNEGKGLVPLL 139


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RESULT 6
US-10-953-349-37586
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 37586
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37586
Query Match 30.1%; Score 215; DB 6; Length 113;
Best Local Similarity 45.9%; Pred. No. 1.1e-12;
Matches 45; Conservative 17; Mismatches 32; Indels 4; Gaps 2;
Qy 41 VAHVLDLIGQKEVFAAATYCPYCKATLSTLFOELNVPKSKALVLELDMSGNGSEIQDAL 100
Db 3 LAKAKBIVASAPVVVFSKCPFC-VQVKLFTQLG--ASFKAIELDTSDDGTEIQSAL 58
Qy 101 EETSGQTVPNVYINGKHGNSDLETLKNGKLAEL 138
Db 59 AEWTGQRTVPNVFNGKHGCGDDTIALNKGKLVALL 96
RESULT 7
US-10-953-349-5626
; Sequence 5626, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5626
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5626
Query Match 30.1%; Score 215; DB 6; Length 133;
Best Local Similarity 38.3%; Pred. No. 1.3e-12;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;
Qy 7 FDSNLVIVIIITLAFRIIAKRFSTPKMVSQETVAHVLDLIGQKEVFAAATYCPYCKA 66
Db 2 FRISWMVLLVALVTFTISMVSSAASSPE-----ADFVKTTISSHKIVIFSVCYCKK 55
Qy 67 TLSTLFOELN-VPKSKALVLELDMSGNGSEIQDALEISGQKTVPNVYINGKHGNSDL 125
Db 56 AKS-VFRELDQVP-----YVVELDEREDGWSIQALGEIVGRRTVPQVFINGKHLGSDDT 110
Qy 126 ETLLKNGKLAEL 138
Db 111 VDYESGELAKLL 123
RESULT 8
US-10-953-349-5625
; Sequence 5625, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5625
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5625
Query Match 30.1%; Score 215; DB 6; Length 135;
Best Local Similarity 38.3%; Pred. No. 1.4e-12;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;
Qy 7 FDSNLVIVIIITLAFRIIAKRFSTPKMVSQETVAHVLDLIGQKEVFAAATYCPYCKA 66
Db 4 FRISWMVLLVALVTFTISMVSSAASSPE-----ADFVKTTISSHKIVIFSVCYCKK 57
Qy 67 TLSTLFOELN-VPKSKALVLELDMSGNGSEIQDALEISGQKTVPNVYINGKHGNSDL 125
Db 58 AKS-VFRELDQVP-----YVVELDEREDGWSIQALGEIVGRRTVPQVFINGKHLGSDDT 112
Qy 126 ETLLKNGKLAEL 138
Db 113 VDYESGELAKLL 125
RESULT 9
US-10-953-349-5624
; Sequence 5624, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5624
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5624
Query Match 30.1%; Score 215; DB 6; Length 152;
Best Local Similarity 38.3%; Pred. No. 1.6e-12;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;
Qy 7 FDSNLVIVIIITLAFRIIAKRFSTPKMVSQETVAHVLDLIGQKEVFAAATYCPYCKA 66
Db 21 FRISWMVLLVALVTFTISMVSSAASSPE-----ADFVKTTISSHKIVIFSVCYCKK 74
Qy 67 TLSTLFOELN-VPKSKALVLELDMSGNGSEIQDALEISGQKTVPNVYINGKHGNSDL 125
Db 75 AKS-VFRELDQVP-----YVVELDEREDGWSIQALGEIVGRRTVPQVFINGKHLGSDDT 129
Qy 126 ETLLKNGKLAEL 138
Db 130 VDYESGELAKLL 142
RESULT 10
US-10-449-902-43865
; Sequence 43865, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5625
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5625
Query Match 30.1%; Score 215; DB 6; Length 135;
Best Local Similarity 38.3%; Pred. No. 1.4e-12;
Matches 51; Conservative 28; Mismatches 42; Indels 12; Gaps 4;
Qy 7 FDSNLVIVIIITLAFRIIAKRFSTPKMVSQETVAHVLDLIGQKEVFAAATYCPYCKA 66
Db 4 FRISWMVLLVALVTFTISMVSSAASSPE-----ADFVKTTISSHKIVIFSVCYCKK 57
Qy 67 TLSTLFOELN-VPKSKALVLELDMSGNGSEIQDALEISGQKTVPNVYINGKHGNSDL 125
Db 58 AKS-VFRELDQVP-----YVVELDEREDGWSIQALGEIVGRRTVPQVFINGKHLGSDDT 112
Qy 126 ETLLKNGKLAEL 138
Db 113 VDYESGELAKLL 125
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